



APPLICATION NUMBER: 08/805,117  
 FILING DATE: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BILLINGS, LUCY J.  
 REGISTRATION NUMBER: 36,749  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-855-0555  
 TELEFAX: 415-845-1166  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 121 amino acids  
 TYPE: amino acid  
 -STRANDEDNESS: single  
 TOPOLOGY: linear  
 IMMEDIATE SOURCE:  
 LIBRARY: THYRNOT03  
 CLONE: 14437B  
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
 US-09-904-603-1

Query Match 100.0%; Score 625; DB 24; Length 121;  
 Best Local Similarity 100.0%; Pred. No. 2; e=65;  
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MPSDRPKQRRSADRCKEVQQRDQHPSKIPVITERYKEGKOLPVLDPKTKEFLVDPHNM 60  
 Db 1 MPSDRPKQRRSADRCKEVQQRDQHPSKIPVITERYKEGKOLPVLDPKTKEFLVDPHNM 60  
 Qy 61 SELVKIRRQLQNLPTQAFFLVMQHSMVSVSPIDYQEKEDEGFLYMVVASQETFG 120  
 Db 61 SELVKIRRQLQNLPTQAFFLVMQHSMVSVSPIDYQEKEDEGFLYMVVASQETFG 120  
 Qy 121 F 121  
 Db 121 F 121

RESULT 2  
 PCT-US01-18569-2536  
 ; Sequence 2536, Application PC/TUS0118569  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Human Genome Sciences, Inc.  
 ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
 ; FILE REFERENCE: PAJ33PCT  
 ; CURRENT APPLICATION NUMBER: PCT/US01/18569  
 ; CURRENT FILING DATE: 2001-05-07  
 ; PRIOR APPLICATION NUMBER: 60/209,467  
 ; PRIORITY FILING DATE: 2000-06-07  
 ; NUMBER OF SEQ ID NOS: 4360  
 ; SOFTWARE: Patentin Ver. 2.0  
 ; SEQ ID NO 2536  
 ; LENGTH: 169  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens

Query Match 100.0%; Score 625; DB 28; Length 169;  
 Best Local Similarity 100.0%; Pred. No. 3; e=65;  
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MPSDRPKQRRSADRCKEVQQRDQHPSKIPVITERYKEGKOLPVLDPKTKEFLVDPHNM 60  
 Db 49 MPSDRPKQRRSADRCKEVQQRDQHPSKIPVITERYKEGKOLPVLDPKTKEFLVDPHNM 108  
 Qy 61 SELVKIRRQLQNLPTQAFFLVMQHSMVSVSPIDYQEKEDEGFLYMVVASQETFG 120  
 Db 109 SELVKIRRQLQNLPTQAFFLVMQHSMVSVSPIDYQEKEDEGFLYMVVASQETFG 120  
 Qy 121 F 121  
 Db 169 F 169

RESULT 3  
 US-10-264-049-2536  
 ; Sequence 2536, Application US/10264049  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Blise et al.  
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
 ; FILE REFERENCE: PAJ33P1  
 ; CURRENT APPLICATION NUMBER: US/10/264,049  
 ; CURRENT FILING DATE: 2002-10-04  
 ; PRIOR APPLICATION NUMBER: PCT/US01/18569  
 ; PRIOR FILING DATE: 2001-06-07  
 ; PRIORITY APPLICATION NUMBER: US 60/209,467  
 ; NUMBER OF SEQ ID NOS: 4360  
 ; SOFTWARE: Patentin Ver. 3.1  
 ; SEQ ID NO 2536  
 ; LENGTH: 169  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens

Query Match 100.0%; Score 625; DB 28; Length 169;  
 Best Local Similarity 100.0%; Pred. No. 3; e=65;  
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MPSDRPKQRRSADRCKEVQQRDQHPSKIPVITERYKEGKOLPVLDPKTKEFLVDPHNM 60  
 Db 49 MPSDRPKQRRSADRCKEVQQRDQHPSKIPVITERYKEGKOLPVLDPKTKEFLVDPHNM 108  
 Qy 61 SELVKIRRQLQNLPTQAFFLVMQHSMVSVSPIDYQEKEDEGFLYMVVASQETFG 120  
 Db 109 SELVKIRRQLQNLPTQAFFLVMQHSMVSVSPIDYQEKEDEGFLYMVVASQETFG 120  
 Qy 121 F 121  
 Db 169 F 169

RESULT 4  
 PCT-US01-08631-40152  
 ; Sequence 40152, Application PC/TUS0108631  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hyseq, Inc.  
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
 ; FILE REFERENCE: 21272-049  
 ; CURRENT APPLICATION NUMBER: PCT/US01/08631  
 ; CURRENT FILING DATE: 2001-03-30  
 ; PRIOR APPLICATION NUMBER: 09/5540,217  
 ; PRIOR FILING DATE: 2000-03-31  
 ; PRIOR APPLICATION NUMBER: 09/649,167  
 ; PRIOR FILING DATE: 2000-08-23  
 ; NUMBER OF SEQ ID NOS: 60736  
 ; SOFTWARE: Custom  
 ; SEQ ID NO 40152  
 ; LENGTH: 199  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (1)..(199)  
 ; OTHER INFORMATION: Xaa = x or \* as defined in Table 2

Query Match 100.0%; Score 625; DB 1; Length 169;  
 Best Local Similarity 100.0%; Pred. No. 3; e=65;  
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MPSDRPKQRRSADRCKEVQQRDQHPSKIPVITERYKEGKOLPVLDPKTKEFLVDPHNM 60  
 Db 49 MPSDRPKQRRSADRCKEVQQRDQHPSKIPVITERYKEGKOLPVLDPKTKEFLVDPHNM 108  
 Qy 61 SELVKIRRQLQNLPTQAFFLVMQHSMVSVSPIDYQEKEDEGFLYMVVASQETFG 120  
 Db 109 SELVKIRRQLQNLPTQAFFLVMQHSMVSVSPIDYQEKEDEGFLYMVVASQETFG 168  
 Qy 121 F 121  
 Db 169 F 169

Query Match 100.0%; Score 625; DB 1; Length 199;  
 Best Local Similarity 100.0%; Pred. No. 4; e=65;  
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MPSDRPKQRRSADRCKEVQQRDQHPSKIPVITERYKEGKOLPVLDPKTKEFLVDPHNM 60  
 Db 52 MPSDRPKQRRSADRCKEVQQRDQHPSKIPVITERYKEGKOLPVLDPKTKEFLVDPHNM 111



;

FEATURE: ;

NAME/KEY: UNSURE

LOCATION: 105

OTHER INFORMATION: xaa = Glu, Gln

US-60-197-873-14523

Query Match 87.2%; Score 545; DB 31; Length 107; Best Local Similarity 99.1%; Pred. No. 5.8e-56; Matches 106; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPSDRPKKORRSFADRCKEVOQIRDQHPSKIPVITERYKEGKOLPVLDKTKFLVPHVM 60

Db 1 MPSDRPKKORRSFADRCKEVOQIRDQHPSKIPVITERYKEGKOLPVLDKTKFLVPHVM 60

QY 61 SELVKIRRQLQNLNQSTPIADYEQEKEDEGFLYMYASQETFG 107

Db 61 SELVKIRRQLQNLNQSTPIADYEQEKEDEGFLYMYASQETFG 107

;

RESULT 9 ;

US-09-834-366-15699 ;

Sequence 15699, Application US/09834366

GENERAL INFORMATION: ;

APPLICANT: Bejanin, Stephane

APPLICANT: Tanaka, Hiroaki

APPLICANT: Dumas, Milne Edwards, Jean Baptiste

APPLICANT: Jobert, Severin

APPLICANT: Giordano, Jean-Yves

TITLE OF INVENTION: ESTs and Encoded Human Proteins.

FILE REFERENCE: 81.US2.REG

CURRENT APPLICATION NUMBER: US/09/834,366

CURRENT FILING DATE: 2001-04-13

PRIOR APPLICATION NUMBER: US 60/197,873

PRIOR FILING DATE: 2000-04-18

NUMBER OF SEQ ID NOS: 52153

SOFTWARE: Patent.pm

SEQ ID NO 15699

TYPE: PRT

ORGANISM: Homo sapiens

US-09-834-366-15699

;

Query Match 83.4%; Score 521; DB 23; Length 123; Best Local Similarity 82.5%; Pred. No. 5e-53; Matches 99; Conservative 12; Mismatches 9; Indels 0; Gaps 0;

QY 1 MPSDRPKKORRSFADRCKEVOQIRDQHPSKIPVITERYKEGKOLPVLDKTKFLVPHVM 60

Db 1 MPSDRPKKORRSFADRCKEVOQIRDQHPSKIPVITERYKEGKOLPVLDKTKFLVPHVM 60

QY 61 SELVKIRRQLQNLNQSTPIADYEQEKEDEGFLYMYASQETFG 120

Db 61 SELVKIRRQLQNLNQSTPIADYEQEKEDEGFLYMYASQETFG 120

;

RESULT 10 ;

US-60-197-873-15699 ;

Sequence 15699, Application US/60197873

GENERAL INFORMATION: ;

APPLICANT: Bejanin, Stephane

APPLICANT: Tanaka, Hiroaki

APPLICANT: Dumas, Milne Edwards, Jean Baptiste

APPLICANT: Jobert, Severin

APPLICANT: Giordano, Jean-Yves

TITLE OF INVENTION: ESTs and Encoded Human Proteins.

CURRENT APPLICATION NUMBER: US/60/197,873

CURRENT FILING DATE: 2000-04-18

NUMBER OF SEQ ID NOS: 52153

SOFTWARE: Patent.pm

SEQ ID NO 15699

TYPE: PRT

;

RESULT 11 ;

US-09-488-725A-2805 ;

Sequence 2805, Application US/09488725A

GENERAL INFORMATION: ;

APPLICANT: Hysed Inc

TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides

FILE REFERENCE: 7841LPCT

CURRENT APPLICATION NUMBER: US/09/488-725A

CURRENT FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: US/09/488-725

PRIOR FILING DATE: 2000-01-21

PRIOR APPLICATION NUMBER: US09/552,317

PRIOR FILING DATE: 2000-04-25

PRIOR APPLICATION NUMBER: US09/598,042

PRIOR FILING DATE: 2000-06-20

PRIOR APPLICATION NUMBER: US09/620,312

PRIOR FILING DATE: 2000-07-19

PRIOR APPLICATION NUMBER: US09/653,450

PRIOR FILING DATE: 2000-08-31

PRIOR APPLICATION NUMBER: US09/662,191

PRIOR FILING DATE: 2000-09-14

PRIOR APPLICATION NUMBER: US09/693,036

PRIOR FILING DATE: 2000-10-19

PRIOR APPLICATION NUMBER: US09/727,344

PRIOR FILING DATE: 2000-11-29

NUMBER OF SEQ ID NOS: 744

SOFTWARE: pt\_FL\_genes\_b Versions 1.0

SEQ ID NO 2805

LENGTH: 126

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TYPE: PRT

ORGANISM: Homo sapiens

US-09-488-725A-2805

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Query Match 83.4%; Score 521; DB 18; Length 125; Best Local Similarity 82.5%; Pred. No. 5.1e-53; Matches 99; Conservative 12; Mismatches 9; Indels 0; Gaps 0;

QY 1 MPSDRPKKORRSFADRCKEVOQIRDQHPSKIPVITERYKEGKOLPVLDKTKFLVPHVM 60

Db 1 MPSDRPKKORRSFADRCKEVOQIRDQHPSKIPVITERYKEGKOLPVLDKTKFLVPHVM 60

QY 61 SELVKIRRQLQNLNQSTPIADYEQEKEDEGFLYMYASQETFG 120

Db 61 SELVKIRRQLQNLNQSTPIADYEQEKEDEGFLYMYASQETFG 120

;

RESULT 12 ;

US-09-834-366-20036 ;

Sequence 20036, Application US/09834366

GENERAL INFORMATION: ;

APPLICANT: Bejanin, Stephane

APPLICANT: Tanaka, Hiroaki

APPLICANT: Dumas, Milne Edwards, Jean Baptiste

APPLICANT: Jobert, Severin

APPLICANT: Giordano, Jean-Yves

TITLE OF INVENTION: ESTs and Encoded Human Proteins.

FILE REFERENCE: 81.US2.REG

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; CURRENT APPLICATION NUMBER: US/09/834,366
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/197,873
; PRIOR FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 52153
; SOFTWARE: Patent.pn
; SEQ ID NO: 20036
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-834-166-20036

RESULT 13
Query Match 83.4%; Score 521; DB 23; Length 125;
Best Local Similarity 82.5%; Pred. No. 5.1e-53; Matches 99; Conservative 12; Mismatches 9; Indels 0; Gaps 0;
Qy 1 MPSDRFKQRKSFA DRKEVQI DPKVPLDKT KFLVPHNM 60
Db 1 MPS EKTFKQRKF E QVFDVRLR E HPTKLPVIL RYK G E K Q K Q P V L D K T K F L V P H N M 60
Qy 61 SELVKIRRQLN P T Q A F F L V N Q H M S V S T P I A D I Y Q E K D E G F L V A V Y A S Q E T F G 120
Db 61 SELIKIIRRQLN Q A F F L V N Q H M S V S T P I S E V Y E S K E D E G F L I M V Y A S E T F G 120
; US-10-219-051B-7991
; Sequence 7991, Application US/10219051B
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation doing business as Massachusetts General
; APPLICANT: Hospital / Bayer AG
; TITLE OF INVENTION: Nucleotide sequences involved in pain
; FILE REFERENCE: LGA 33563 Foreign Countries
; CURRENT APPLICATION NUMBER: US 60/312,147
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/346,382
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: US 60/333,347
; PRIOR FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 14715
; SOFTWARE: Perl script
; SEQ ID NO: 7991
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: RefSeq / NP_073729
; US-10-219-051B-7991

RESULT 14
Query Match 83.4%; Score 521; DB 28; Length 125;
Best Local Similarity 82.5%; Pred. No. 5.1e-53; Matches 99; Conservative 12; Mismatches 9; Indels 0; Gaps 0;
Qy 1 MPSDRFKQRKSFA DRKEVQI DPKVPLDKT KFLVPHNM 60
Db 1 MPS EKTFKQRKF E QVFDVRLR E HPTKLPVIL RYK G E K Q K Q P V L D K T K F L V P H N M 60
Qy 61 SELVKIRRQLN P T Q A F F L V N Q H M S V S T P I A D I Y Q E K D E G F L V A V Y A S Q E T F G 120
Db 61 SELIKIIRRQLN Q A F F L V N Q H M S V S T P I S E V Y E S K E D E G F L I M V Y A S E T F G 120
; US-10-219-051B-13087
; Sequence 13087, Application US/10219051B
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation doing business as Massachusetts General
; APPLICANT: Hospital / Bayer AG
; TITLE OF INVENTION: Nucleotide sequences involved in pain
; FILE REFERENCE: LGA 33563 Foreign Countries

RESULT 15
Query Match 83.4%; Score 521; DB 28; Length 125;
Best Local Similarity 82.5%; Pred. No. 5.1e-53; Matches 99; Conservative 12; Mismatches 9; Indels 0; Gaps 0;
Qy 1 MPSDRFKQRKSFA DRKEVQI DPKVPLDKT KFLVPHNM 60
Db 1 MPS EKTFKQRKF E QVFDVRLR E HPTKLPVIL RYK G E K Q K Q P V L D K T K F L V P H N M 60
Qy 61 SELVKIRRQLN P T Q A F F L V N Q H M S V S T P I A D I Y Q E K D E G F L V A V Y A S Q E T F G 120
Db 61 SELIKIIRRQLN Q A F F L V N Q H M S V S T P I S E V Y E S K E D E G F L I M V Y A S E T F G 120
; US-60-197-873-20036
; Sequence 20036, Application US/60197873
; GENERAL INFORMATION:
; APPLICANT: Bejamin, Stephanie
; APPLICANT: Tanaka, Hiroaki
; APPLICANT: Dumas, Mire Edmaris, Jean Baptiste
; APPLICANT: Jobert, Severin
; APPLICANT: Giordano, Jean-Yves
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: 81 US1, PRO
; CURRENT APPLICATION NUMBER: US/60/197,873
; CURRENT FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 52153
; SOFTWARE: Patent.pn
; SEQ ID NO: 20036
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-60-197-873-20036

RESULT 16
Query Match 83.4%; Score 521; DB 31; Length 125;
Best Local Similarity 82.5%; Pred. No. 5.1e-53; Matches 99; Conservative 12; Mismatches 9; Indels 0; Gaps 0;
Qy 1 MPSDRFKQRKSFA DRKEVQI DPKVPLDKT KFLVPHNM 60
Db 1 MPS EKTFKQRKF E QVFDVRLR E HPTKLPVIL RYK G E K Q K Q P V L D K T K F L V P H N M 60
Qy 61 SELVKIRRQLN P T Q A F F L V N Q H M S V S T P I A D I Y Q E K D E G F L V A V Y A S Q E T F G 120
Db 61 SELIKIIRRQLN Q A F F L V N Q H M S V S T P I S E V Y E S K E D E G F L I M V Y A S E T F G 120
; US-60-197-873-20036
; Sequence 20036, Application US/60197873
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation doing business as Massachusetts General
; APPLICANT: Hospital / Bayer AG
; TITLE OF INVENTION: Nucleotide sequences involved in pain
; FILE REFERENCE: LGA 33563 Foreign Countries

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Search completed: August 11, 2003, 10:24:10

Job time : 375 secs

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 (without alignments)  
 115,496 Million cell updates/sec

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OM protein - protein search, using sw model

Title: US-09-904-603-1  
 Perfect score: 1  
 Sequence: MPSDRPKKRRSSFADRCKEV. .... ERKEDGFLYMWVASYQETFGF 121

Scoring table: BL0SUM62  
 Gapcp 10.0 , Gapext 0.5

Searched: 98705 sqs, 2044758 residues

Total number of hits satisfying chosen parameters: 98705

Minimum DB seq length: 0  
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%, Maximum Match 100%  
 Listing first 45 summaries

Database : Pending\_Patents\_AA\_New,\*  
 1: /cgp2\_6/ptodata/1/paa/PCT\_NEW\_COMBO.pep: \*  
 2: /cgp2\_6/ptodata/1/paa/US06\_NEW\_COMBO.pep: \*  
 3: /cgp2\_6/ptodata/1/paa/US07\_NEW\_COMBO.pep: \*  
 4: /cgp2\_6/ptodata/1/paa/US08\_NEW\_COMBO.pep: \*  
 5: /cgp2\_6/ptodata/1/paa/US09\_NEW\_COMBO.pep: \*  
 6: /cgp2\_6/ptodata/1/paa/US10\_NEW\_COMBO.pep: \*  
 7: /cgp2\_6/ptodata/1/paa/US60\_NEW\_COMBO.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result No.	Score	Query	Length	DB	ID	Description
1	521	83.4	125	6	US-10-286-897-2805	Sequence 2805, AP
2	521	83.4	155	6	US-10-286-897-6317	Sequence 6317, AP
3	411	65.8	222	6	US-10-273-573-6982	Sequence 6982, AP
4	301	48.2	120	6	US-10-293-244-3825	Sequence 3825, AP
5	272	43.5	135	5	US-10-293-244-1857	Sequence 1857, AP
6	256	41.0	50	5	US-09-820-649-221	Sequence 221, APP
7	235	37.8	46	5	US-09-820-649-222	Sequence 222, APP
8	203	32.5	117	6	US-10-408-765A-0121	Sequence 0121, APP
9	193	30.9	133	6	US-10-603-113-14574	Sequence 14574, APP
10	68.5	11.0	602	6	US-10-451-901-4	Sequence 4, APP
11	68.5	11.0	1648	6	US-10-603-113-14286	Sequence 14286, APP
12	68	10.9	243	6	US-10-617-320-4644	Sequence 4644, APP
13	68	10.9	1619	6	US-09-820-843B-16	Sequence 16, APP
14	66.5	10.6	469	6	US-10-603-113-15278	Sequence 15278, APP
15	66	10.6	454	6	US-10-603-113-17078	Sequence 17078, APP
16	65.5	10.5	283	6	US-10-603-113-21629	Sequence 21629, APP
17	65.5	10.5	322	6	US-10-326-956-267	Sequence 267, APP
18	65.5	10.5	1178	6	US-10-326-956-2805	Sequence 2805, APP
19	65.5	10.5	2000	6	US-10-326-956-339	Sequence 339, APP
20	65.5	10.5	4910	6	US-10-346-863-21	Sequence 21, APP
21	65	10.4	1047	6	US-10-326-956-2653	Sequence 2653, APP
22	65	10.4	3058	7	US-60-487-610-501	Sequence 2541, APP
23	64.5	10.3	655	6	US-10-326-956-483	Sequence 483, APP
24	64	10.2	308	6	US-10-294-433-233	Sequence 233, APP
25	63.5	10.2	303	6	US-10-617-320-4703	Sequence 4703, APP
26	63	10.1	45	5	US-09-820-649-220	Sequence 220, APP

**ALIGNMENTS**

RESULT 1  
 US-10-286-897-2805  
 Sequence 2805, Application US/1u286897  
 GENERAL INFORMATION:  
 APPLICANT: Hyseq Inc  
 TITLE OF INVENTION: Novel Nucleic Acid and Poly  
 FILE REFERENCE: 7841PCT  
 CURRENT APPLICATION NUMBER: US/1u10/286, 897  
 CURRENT FILING DATE: 2002-11-01  
 PRIOR APPLICATION NUMBER: US/09/488, 725  
 PRIOR FILING DATE: 2000-01-21  
 PRIOR APPLICATION NUMBER: US/09/552, 317  
 PRIOR FILING DATE: 2000-04-25  
 PRIOR APPLICATION NUMBER: US/09/598, 042  
 PRIOR FILING DATE: 2000-06-20  
 PRIOR APPLICATION NUMBER: US/09/620, 312  
 PRIOR FILING DATE: 2000-07-19  
 PRIOR APPLICATION NUMBER: US/09/653, 450  
 PRIOR FILING DATE: 2000-08-31  
 PRIOR APPLICATION NUMBER: US/09/662, 191  
 PRIOR FILING DATE: 2000-09-14  
 PRIOR APPLICATION NUMBER: US/09/6593, 036  
 PRIOR FILING DATE: 2000-10-19  
 PRIOR APPLICATION NUMBER: US/09/727, 344  
 PRIOR FILING DATE: 2000-11-29  
 NUMBER OF SEQ ID NOS: 7143  
 SOFTWARE: pt\\_FL\\_genes\\_b Versions 1.0  
 SEQ ID NO: 2805  
 LENGTH: 125  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-286-897-2805

Query Match 83.4%; Score 521; DB Best local Similarity 82.5%; Pred. No. 2. 1e-5  
 Matches 99; Conservative 12; Mismatches 0

QY 1 MPSDRPKKRRSSFADRCKEV. .... ERKEDGFLYMWVASYQETFGF  
 1 MPSDRPKKRRSSFADRCKEV. .... ERKEDGFLYMWVASYQETFGF

QY 61 SELVKIIPKRLQINPNTQAFLLVNGHMSVSVSPTIA  
 1 SELVKIIPKRLQINPNTQAFLLVNGHMSVSVSPTIA

RESULT 2  
 US-10-286-897-6377  
 Sequence 6377, Application US/10286897

GENERAL INFORMATION:  
 APPLICANT: Hyseq Inc.  
 TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides  
 FILE REFERENCE: 784FLPCT  
 CURRENT APPLICATION NUMBER: US/10/286,897  
 CURRENT FILING DATE: 2002-11-01  
 PRIOR APPLICATION NUMBER: US/09/488,725  
 PRIOR FILING DATE: 2000-01-21  
 PRIOR APPLICATION NUMBER: US/09/552,317  
 PRIOR APPLICATION NUMBER: US/09/598,042  
 PRIOR FILING DATE: 2000-04-25  
 PRIOR APPLICATION NUMBER: US/09/620,312  
 PRIOR FILING DATE: 2000-06-20  
 PRIOR APPLICATION NUMBER: US/09/653,450  
 PRIOR APPLICATION NUMBER: US/09/662,191  
 PRIOR FILING DATE: 2000-08-31  
 PRIOR APPLICATION NUMBER: US/09/693,036  
 PRIOR FILING DATE: 2000-10-19  
 PRIOR APPLICATION NUMBER: US/09/727,344  
 PRIOR FILING DATE: 2000-11-29  
 NUMBER OF SEQ ID NOS: 7143  
 SOFTWARE: pr\_fl\_genes\_b Versions 1.0  
 SEQ ID NO: 6377  
 LENGTH: 155  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 ;US-10-286-897-6377

RESULT 3  
 US-10-273-573-6982  
 ; Sequence 6982, Application US/10273573  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hyseq, Inc.  
 ; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES  
 ; FILE REFERENCE: 21272-029  
 ; CURRENT APPLICATION NUMBER: US/10/293,244  
 ; CURRENT FILING DATE: 2002-11-12  
 ; PRIOR APPLICATION NUMBER: Not Yet Assigned  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: 09/728,422  
 ; PRIOR FILING DATE: 2000-11-30  
 ; PRIOR APPLICATION NUMBER: 09/693,325  
 ; PRIOR FILING DATE: 2000-10-20  
 ; PRIOR APPLICATION NUMBER: 09/663,561  
 ; PRIOR FILING DATE: 2000-09-15  
 ; PRIOR APPLICATION NUMBER: 09/654,936  
 ; PRIOR FILING DATE: 2000-09-01  
 ; PRIOR APPLICATION NUMBER: 09/620,325  
 ; PRIOR FILING DATE: 2000-07-19  
 ; PRIOR APPLICATION NUMBER: 09/598,075  
 ; PRIOR FILING DATE: 2000-06-20  
 ; PRIOR APPLICATION NUMBER: 09/560,875  
 ; PRIOR FILING DATE: 2000-04-27  
 ; PRIOR APPLICATION NUMBER: 09/496,914  
 ; NUMBER OF SEQ ID NOS: 3960  
 ; SOFTWARE: Custom  
 ; SEQ ID NO: 3825  
 ; LENGTH: 120  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ;US-10-293-244-3825

Query Match 65.0%; Score 411; DB 6; Length 222;  
 Best Local Similarity 67.2%; Pred. No. 9.1e-39; Matches 82; Conservative 16; Mismatches 22; Indels 2; Gaps 2;  
 Matches 82; Conservative 16; Mismatches 22; Indels 2; Gaps 2;  
 QY 1 MPSDRFKKRSFADDCKEYKQVQIRDQHPSKIP-VIILERGEGKQFLVQFLDKRKFVLPDHVN 59  
 Db 32 MPEKTFKQRTFQEQRVEDVFLRQEHPQTIPRXLERSKGNNOPPVLDKTFKFLVDPDHVN 91  
 QY 60 MSELVKIRRLQNLNTQAFFLWNQHSMVSYST-PIADYQEKEQEDGFLYMWVAAQET 118  
 Db 92 MSELVKIRRLQNLNTQAFFLWNQHSMVSYSPHIESEKEQEDGFLYMWVCCPPE 151  
 QY 119 FG 120  
 Db 152 YG 153

RESULT 4  
 US-10-293-244-3825  
 ; Sequence 3825, Application US/10293244  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hyseq, Inc.  
 ; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides  
 ; FILE REFERENCE: 21272-029  
 ; CURRENT APPLICATION NUMBER: US/10/293,244  
 ; CURRENT FILING DATE: 2002-11-12  
 ; PRIOR APPLICATION NUMBER: Not Yet Assigned  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: 09/728,422  
 ; PRIOR FILING DATE: 2000-11-30  
 ; PRIOR APPLICATION NUMBER: 09/693,325  
 ; PRIOR FILING DATE: 2000-10-20  
 ; PRIOR APPLICATION NUMBER: 09/663,561  
 ; PRIOR FILING DATE: 2000-09-15  
 ; PRIOR APPLICATION NUMBER: 09/654,936  
 ; PRIOR FILING DATE: 2000-09-01  
 ; PRIOR APPLICATION NUMBER: 09/620,325  
 ; PRIOR FILING DATE: 2000-07-19  
 ; PRIOR APPLICATION NUMBER: 09/598,075  
 ; PRIOR FILING DATE: 2000-06-20  
 ; PRIOR APPLICATION NUMBER: 09/560,875  
 ; PRIOR FILING DATE: 2000-04-27  
 ; PRIOR APPLICATION NUMBER: 09/496,914  
 ; NUMBER OF SEQ ID NOS: 3960  
 ; SOFTWARE: Custom  
 ; SEQ ID NO: 3825  
 ; LENGTH: 120  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ;US-10-293-244-3825

Query Match 48.2%; Score 301; DB 6; Length 120;  
 Best Local Similarity 59.2%; Pred. No. 8.2e-27; Matches 58; Conservative 16; Mismatches 24; Indels 0; Gaps 0;  
 Matches 58; Conservative 16; Mismatches 24; Indels 0; Gaps 0;  
 QY 23 IRDQHPSKIP-VIILERGEGKQFLVQFLDKRKFVLPDHVNMSLVLKIRRLQNLNTQAFFL 82  
 Db 2 IRAKFNPKIPVVERYPRETFLLPPLKTKFLVPOETLTMFLSIRSMLRATEAFL 61  
 QY 83 VNQHSMVSYSTPIADYQEKEQEDGFLYMWVAAQET 120  
 Db 62 VNQHSMVSYSTPIADYQEKEQEDGFLYMWVAAQET 99

RESULT 5  
 US-10-293-244-1857  
 ; Sequence 1857, Application US/10293244  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hyseq, Inc.  
 ; APPLICANT: Tang, Y. Tom et al

OTHER INFORMATION: PROSTANOID EP1 RECEPTOR SIGNATURE domain identified by  
 OTHER INFORMATION: eMATRIX, accession number PR0580E, p-value=2.014e-10, raw score  
 OTHER INFORMATION: 7.15  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (1)..(22)  
 OTHER INFORMATION: xaa = x or \* as defined in Table 2.  
 ;US-10-273-573-6982

TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides  
 FILE REFERENCE: 21272-029  
 CURRENT APPLICATION NUMBER: US/10/293,244  
 CURRENT FILING DATE: 2002-11-12  
 PRIOR APPLICATION NUMBER: Not yet Assigned  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: 09/728,422  
 PRIOR FILING DATE: 2000-11-30  
 PRIOR APPLICATION NUMBER: 09/663,325  
 PRIOR FILING DATE: 2000-09-20  
 PRIOR APPLICATION NUMBER: 09/663,561  
 PRIOR FILING DATE: 2000-09-15  
 PRIOR APPLICATION NUMBER: 09/654,936  
 PRIOR FILING DATE: 2000-09-01  
 PRIOR APPLICATION NUMBER: 09/620,325  
 PRIOR FILING DATE: 2000-07-19  
 PRIOR APPLICATION NUMBER: 09/598,075  
 PRIOR FILING DATE: 2000-05-20  
 PRIOR APPLICATION NUMBER: 09/560,875  
 PRIOR FILING DATE: 2000-04-27  
 PRIOR APPLICATION NUMBER: 09/496,914  
 PRIOR FILING DATE: 2000-02-03  
 NUMBER OF SEQ ID NOS: 3960  
 SOFTWARE: Custom  
 SEQ ID NO: 1857  
 LENGTH: 135  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-244-244-1857

RESULT 6  
 Query Match 43.5%; Score 272; DB 6; Length 135;  
 Best Local Similarity 55.6%; Pred. No. 1.7e-23;  
 Matches 55; Conservative 18; Mismatches 0; Gaps 0;  
 Indels 0; Software: Custom

QY 1 MPSDRPKKRSFADRCKEQQIQRDQHESKIPVIERKGEKQLPVLDKTKFLVPHVNMSELVKIIRRLQINP 60  
 Db 7 IPSVPRPKKRSFADRCKEQQIQRDQHESKIPVIERKGEKQLPVLDKTKFLVPHVNMSELVKIIRRLQINP 65

QY 61 SELVKIIRRQLNQIQAFFLVMNOHSMVSVSPTRADIY 99  
 Db 67 TQFLSIIRSRMVLRAEAYFLVYVNLKSLVMSATMAEY 105

RESULT 7  
 US-09-820-649-221  
 Query Match 41.0%; Score 256; DB 5; Length 50;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-22;  
 Matches 50; Conservative 0; Mismatches 0; Gaps 0;  
 Indels 0; Software: Custom

QY 26 QHPSKIPVIERKGEKQLPVLDKTKFLVPHVNMSELVKIIRRLQINP 75  
 Db 1 QHPSKIPVIERKGEKQLPVLDKTKFLVPHVNMSELVKIIRRLQINP 80

RESULT 8  
 US-09-820-649-222  
 Query Match 37.8%; Score 245; DB 5; Length 46;  
 Best Local Similarity 100.0%; Pred. No. 4.3e-20;  
 Matches 46; Conservative 0; Mismatches 0; Gaps 0;  
 Indels 0; Software: Custom

QY 76 TQAFFLVLVHSMVSVSPTRADIYKEDGFLYMMWYASOEFQFG 121  
 Db 1 TQAFFLVLVHSMVSVSPTRADIYKEDGFLYMMWYASOEFQFG 126

PRIOR APPLICATION NUMBER: PCT/US98/15949  
 PRIOR FILING DATE: 1998-07-29  
 PRIOR APPLICATION NUMBER: 60/054,212  
 PRIOR FILING DATE: 1997-07-30  
 PRIOR APPLICATION NUMBER: 60/054,209  
 PRIOR FILING DATE: 1997-07-30  
 PRIOR APPLICATION NUMBER: 60/054,234  
 PRIOR FILING DATE: 1997-07-30  
 PRIOR APPLICATION NUMBER: 60/054,218  
 PRIOR FILING DATE: 1997-07-30  
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 PRIOR FILING DATE: 1997-07-30  
 PRIOR APPLICATION NUMBER: 60/054,212  
 PRIOR FILING DATE: 1997-07-30  
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 PRIOR APPLICATION NUMBER: 60/054,215  
 PRIOR FILING DATE: 1997-07-30  
 PRIOR APPLICATION NUMBER: 60/054,211  
 PRIOR FILING DATE: 1997-07-30  
 Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 353  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO: 222  
 ; LENGTH: 46  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-820-649-222

RESULT 9  
 US-10-408-765A-1021  
 Query Match 37.8%; Score 245; DB 5; Length 46;  
 Best Local Similarity 100.0%; Pred. No. 4.3e-20;  
 Matches 46; Conservative 0; Mismatches 0; Gaps 0;  
 Indels 0; Software: Custom

QY 76 TQAFFLVLVHSMVSVSPTRADIYKEDGFLYMMWYASOEFQFG 121  
 Db 1 TQAFFLVLVHSMVSVSPTRADIYKEDGFLYMMWYASOEFQFG 126

Remaining Prior Application data removed - See File Wrapper or PALM.





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Matches 31; Conservative 22; Mismatches 39; Indels 31; Gaps 8;
Oy 16 RCKEVDQI-RDQHPSKIPVITYRKER---QLVLDKTKFLV--PDHVNMSELVKI 66
Db 159 RSHQVEKLNFNEKFINTPIISSLSPNGSKPPTDLP--DQLEDLIVASPDYNTCTTILT 216
Oy 67 IRRR---LQLNPTQAFF---LLVQHMSMSVSTIADIVEQEKEQDGFLYMVASQET 118
Db 217 IHDPPEIWANTNPNTGVIETNSTMVLHPLVQ---IMDKIQKEKPE-----NQEK 264
Qy 119 FGF 121
Db 265 FGF 267

RESULT 15
US-10-603-113-17078
; Sequence 17078 Application US/10603113
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/10/603,113
; CURRENT FILING DATE: 2003-06-24
; PRIOR APPLICATION NUMBER: US/09/248,796
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 28206
; SEQ ID NO: 17078
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Candida albicans
; US-10-603-113-17078

Query Match 10.6%; score 66; DB 6; Length 454;
Best Local Similarity 22.7%; Pred. No. 9.1; Mismatches 25; Conservative 21; Mismatches 54; Indels 10; Gaps 1; Matches 25;
Oy 8 KQRSSFADRCKEQQTIRDQHPSKIPVITYRKERKGKOLPVLDKTKFLVDPDHVNMSSELVKI 67
Db 233 KYPKEASRLK-----NKLSTRPYCGGGESTLVLTRLRPLIAERTDHHLLII 282
Oy 68 RRLRLQMLPTQAFLLVNLQHMSMSVSTIADIYEQEKEQDGFLYMVASQE 117
Db 283 SHRVVSRILLAYFLNLDKSAIGELDWPFLHTLCLHHPYGDYTMYEDE 332

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GenCore version 5.1.6  
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CM nucleic - nucleic search, using sw model

run on: August 15, 2003, 08:09:17 : Search time 2934 Seconds

7147.724 Million cell updates/sec

Title: US-09-904-603-2

Perfect score: 640

Sequence: 1 GTCGGCAGCGCAAGCGCC.....GCCGCGCTAGTCAGAAGGCA 640

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 32997241 seqs, 168392548 residues

Total number of hits satisfying chosen parameters: 65994482

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending\_Patents\_NA\_Main:\*

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2: /cgn2\_6/ptodata/1/pna/PECTUS\_COMBO.seq.old:\*

3: /cgn2\_6/ptodata/1/pna/US06\_06\_COMBO.seq:\*

4: /cgn2\_6/ptodata/1/pna/US07\_COMBO.seq:\*

5: /cgn2\_6/ptodata/1/pna/US08\_06\_COMBO.seq:\*

6: /cgn2\_6/ptodata/1/pna/US081\_COMBO.seq:\*

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35: /cgn2\_6/ptodata/1/pna/US098A\_COMBO.seq:\*

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37: /cgn2\_6/ptodata/1/pna/US098D\_COMBO.seq:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No. Score Match length 1K 10

Description

Result No.	Score	Match length	1K	10	Description
1	640	100	640	38	Sequence 2, AP4
2	627.4	98.0	925	95	Sequence 545, AP
3	627.4	98.0	945	47	Sequence 546, AP
4	627.4	98.0	977	21	Sequence 1555, AP

## ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36-749

REFERENCE/DOCKET NUMBER: PF-0211 US

## TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-0555

## TELEFAX: 415-845-4166

TELEX: &lt;Unknown&gt;

## INFORMATION FOR SEQ ID NO: 2:

## SEQUENCE CHARACTERISTICS:

LENGTH: 640 base pairs

## TYPE: nucleic acid

## STRANDEDNESS: single

## TOPOLOGY: linear

## IMMEDIATE SOURCE:

LIBRARY: THYRNOT03

## CLONE: 1441378

## SEQUENCE DESCRIPTION:

SEQ ID NO: 2:

US-09-904-603-2

Query Match 100 %; Score 640; DB 38; Length 640;

Best Local Similarity 100 %; Pred No. 1. 6e-109;

Matches 640; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 12073, A  
1 CTCCCCGAGGGAGCCGAGCCGGGGCTGAGCCGAGCCCCGAGGCGCTGAGCCGAGGGCG 60  
Sequence 14761, A  
1 CTCCCCGAGGGAGCCGAGCCGGGGCTGAGCCGAGCCCCGAGGCGCTGAGCCGAGGGCG 60  
Sequence 26466, A  
1 GGAGCCCCGAGCCCCAACCGCAGACATCCCCGGCCAGAGCCCCGGCC 120  
Sequence 12073, A  
26 APPI  
Sequence 26, APPI  
Sequence 9784, AP  
Sequence 9784, AP  
Sequence 3509, AP  
61 GGAGCCCCGAGCCCCAACCGCAGACATCCCCGGCCAGAGCCCCGGCC 120  
Sequence 14460, A  
61 GGAGCCCCGAGCCCCAACCGCAGACATCCCCGGCCAGAGCCCCGGCC 120  
Sequence 14460, A  
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Sequence 14460, A  
63 APPI  
Sequence 14460, A  
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Sequence 867, APPI  
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RESULT 4

US-09-471-275-1555

Sequence 1555, Application US/09471275

GENERAL INFORMATION:

APPLICANT: Hyseq, Inc.

TITLE OF INVENTION: Novel Contigs Obtained Title of Invention: From Various Libraries

FILE REFERENCE:

CURRENT APPLICATION NUMBER: US/09/471, 275

CURRENT FILING DATE: 1999-12-23

EARLIER APPLICATION NUMBER: US 09/235, 076

EARLIER FILING DATE: 1999-01-20

EARLIER APPLICATION NUMBER: US 09/234, 611

EARLIER FILING DATE: 1999-01-22

EARLIER APPLICATION NUMBER: US 09/240, 371

EARLIER FILING DATE: 1999-01-29

EARLIER APPLICATION NUMBER: US 09/277, 227

EARLIER FILING DATE: 1999-03-25

EARLIER APPLICATION NUMBER: US 09/271, 490

EARLIER FILING DATE: 1999-03-18

EARLIER APPLICATION NUMBER: US 09/293, 972

EARLIER FILING DATE: 1999-04-15

EARLIER APPLICATION NUMBER: US 09/274, 861

EARLIER FILING DATE: 1999-03-23

EARLIER APPLICATION NUMBER: US 60/125, 453

EARLIER FILING DATE: 1999-03-19

EARLIER APPLICATION NUMBER: US 60/126, 605

EARLIER FILING DATE: 1999-03-26

EARLIER APPLICATION NUMBER: US 09/306, 350

EARLIER FILING DATE: 1999-03-07

EARLIER APPLICATION NUMBER: US 09/399, 720

EARLIER FILING DATE: 1999-09-21

EARLIER APPLICATION NUMBER: US 09/404, 284

EARLIER FILING DATE: 1999-09-21

EARLIER APPLICATION NUMBER: US 09/274, 861

EARLIER FILING DATE: 1999-03-23

EARLIER APPLICATION NUMBER: US 60/125, 453

EARLIER FILING DATE: 1999-03-19

EARLIER APPLICATION NUMBER: US 60/126, 605

EARLIER FILING DATE: 1999-03-26

EARLIER APPLICATION NUMBER: US 09/306, 350

EARLIER FILING DATE: 1999-03-07

EARLIER APPLICATION NUMBER: US 09/399, 720

EARLIER FILING DATE: 1999-09-21

EARLIER APPLICATION NUMBER: US 09/404, 284

EARLIER FILING DATE: 1999-09-21

EARLIER APPLICATION NUMBER: US 09/274, 861

NUMBER OF SEQ ID NOS: 10451

SOFTWARE: pt\_ct\_genes Version 1.0

SEQ ID NO 1555

LENGTH: 977

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc\_feature

LOCATION: (155)..(517)

OTHER INFORMATION: similar to gi455109 in the genepept database release 114, other information: Run with FASTXY 3.3t00, default parameters

US-09-471-275-1555

Query Match

Best Local Similarity 99.0%; Score 627.4; DB 21; Length 977; Matches 639; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

1 CTCCCCGAGCCAGGGCGGCTGCTAGGGAGGCCGAGCCCTGTAGGGAGGGC 60

15 CTCCCCGAGCCAGGGCGGCTGCTAGGGAGGCCGAGCCCTGTAGGGAGGGC 60

15 GGAG-GCCCGAGGCCCAACCGCGACACATCCCGCGGCCAGAGCCGGCT 74

61 GGAG-GCCCGAGGCCCAACCGCGACACATCCCGCGGCCAGAGCCGGCT 74

75 GGAGCCCCGGAGCCCCAACCGCGACACATCCCGCGGCCAGAGCCGGCT 134

120 CGGCGAGCCGGCCGGCCGGCTAGCGCGAGCCGCTTCAGCGAGCGGAGCTTCG 179

135 CGCCCACTCGGCCGCGCTGAGCGCTTCAGCGAGCGGGAGCTTCG 194

180 CGGACCGCTGAGGGATCAGCAGATCCGGACCCAGCCCCAGCAAATCCGGTGA 239

RESULT 5

US-09-488-725B-8516

Sequence 8516, Application US/09488725B

GENERAL INFORMATION:

APPLICANT: Ankura Slinku

APPLICANT: Yuanhua T. Tang

APPLICANT: Chenghua Liu

APPLICANT: Radoje T. Drmanac

TITLE OF INVENTION: Novel Contigs Obtained Title of Invention: From Various Libraries

FILE REFERENCE:

CURRENT APPLICATION NUMBER: US/09/488, 725B

CURRENT FILING DATE: 2000-01-21

PRIOR APPLICATION NUMBER: US 09/004, 182

PRIOR FILING DATE: 1998-01-07

PRIOR APPLICATION NUMBER: US 09/034, 341

PRIOR FILING DATE: 1998-02-13

PRIOR APPLICATION NUMBER: US 09/045, 400

PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: US 09/321, 214

PRIOR FILING DATE: 1999-05-26

PRIOR APPLICATION NUMBER: US 09/131, 598

PRIOR FILING DATE: 1998-08-10

PRIOR APPLICATION NUMBER: US 09/170, 294

PRIOR FILING DATE: 1998-10-13

PRIOR APPLICATION NUMBER: US 09/179, 473

PRIOR FILING DATE: 1998-10-27

PRIOR APPLICATION NUMBER: US 09/181, 430

PRIOR FILING DATE: 1998-10-28

PRIOR APPLICATION NUMBER: US 09/235, 076

PRIOR FILING DATE: 1999-01-20

PRIOR APPLICATION NUMBER: US 09/234, 611

PRIOR FILING DATE: 1999-01-22

Remaining Prior Application data removed - See File Wrapper or PALM

NUMBER OF SEQ ID NOS: 10289

SOFTWARE: pt\_ct\_genes Version 1.0.1

SEQ ID NO 8516

LENGTH: 977

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

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; NAME/KEY: misc_feature
; LOCATION: (155)...(17)
; OTHER INFORMATION: Run with FASTXY 3.3t00, default parameters
; OS-09-48B-725B-8516

Query Match 98.0%; Score 627.4; DB 21; Length 1060;
Best Local Similarity 99.7%; Pred. No. 3.4e-107;
Matches 639; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
Query 1 CTCGGCGAGCGAGCGCGCTGCTAGCGCGAGCGCCCTGAGCGAGCGC; 60
Db 15 CTCCCGAGCGAGCGCGCTGCTAGCGCGAGCGCCCTGAGCGAGCGC; 60
Query 61 GGAG-GCCCGAGGCCCAACCGAGACACATCCCGCCGCCAGAGCCGGCTGCG; 119
Db 75 GGAGGCCCGAGGCCCAACCGAGACACATCCCGCCGCCAGAGCCGGCTGCG; 134
Query 120 CGCCAGCCGGCCCGCGATGCCCTACACGGCTTCAAGAGCGGAGCTCG; 179
Db 145 CGCCAGCCGGCCGCCGCCGCGCAAGCCACAGCCGCTTCAAGAGCGGAGCTCG; 194
Query 180 CGACAGCTGTAAGAGGATAGCAGCATGCCGCGAGCACCCAGCAAAATCCGGTGA; 239
Db 195 CGACCGCTTAAGAGGATAGCAGCATGCCGCGAGCACCCAGCAAAATCCGGTGA; 254
Query 240 TCATGGAGCTACAGGGTGAAGAACGAGCTGGCCGCTCCGGACAGAATTTG; 299
Db 255 TCATGGAGCTACAGGGTGAAGAACGAGCTGGCCGCTCCGGACAGAATTTG; 314
Query 300 TCCGGACCATGTCACATGAGCGAGTGTCAAGATCATCCGGCCCGCTGCGCTG; 359
Db 315 TCCGGACCATGTCACATGAGCGAGTGTCAAGATCATCCGGCCCGCTGCGCTG; 374
Query 360 ACCCGAGCAGCCCTCTCTGCTGCTGTAACGACACACATGGAGCTGACCG; 419
Db 375 ACCCAAGCAGCAGCCCTCTGCTGCTGTAACGACACACATGGAGCTGACCG; 434
Query 420 CCATGGGAGATCTAGGAGCAGGAGAAAGGAGGAGGAGGAGGAGGAGGAGG; 479
Db 435 CCATGGGAGATCTAGGAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG; 494
Query 480 CCTCCAGGAAACCTGGCTCTGAGCCAGTAGGGGCTGGCTGGACTGG; 539
Db 495 CCTCCAGGAAACCTGGCTCTGAGCCAGTAGGGGCTGGCTGGACTGG; 554
Query 540 GGGCCGGTAGGCTGCAAGAGAGCTCTGTTCCGAAGCTGAGCTGCTTACCG; 599
Db 555 GGGCCGGTAGGCTGCAAGAGAGCTCTGTTCCGAAGCTGAGCTGCTTACCG; 614
Query 610 TGGGGCTGGCAGGATGCCCCCTAGTCAGGG3A; 640
Db 615 TGGGGCTGGCAGGATGCCCCCTAGTCAGGG3A; 655

RESULT 6
PCT-US01-18569-361
; Sequence 361, Application PCT/US01/18569
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA13.PCT
; CURRENT APPLICATION NUMBER: PCT/US01/18569
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 361
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo sapiens
; PCT-US01-18569-361

Query Match 98.0%; Score 627.4; DB 2; Length 1000;
Best Local Similarity 99.7%; Pred. No. 3.4e-107;
Matches 639; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
Query 1 CTCGGCGAGCGAGCGCGCTGCTAGCGCGAGCGCCCTGAGCGAGCGC; 60
Db 6 CTCCCGAGCGAGCGCGCTGCTAGCGCGAGCGCCCTGAGCGAGCGC; 65
Query 61 GGAG-GCCCGAGGCCCAACCGAGACACATCCCGCCGCCAGAGCCGGCTGCG; 119
Db 66 GGACCGCCAGGCCCAACCGAGACACATCCCGCCGCCAGAGCCGGCTGCG; 125
Query 120 CGCCAGCCGGCCCGCGATGCCCTACACGGCTTCAAGAGCGGAGCTCG; 179
Db 186 CGACCGCTGTAAGAGGATAGCAGCATGAGCTGGCCGCTCCGGACAGAATTTG; 245
Query 240 TCATGGAGCTACAGGGTGAAGAACGAGCTGGCCGCTCCGGACAGAATTTG; 299
Db 246 TCATGGAGCTACAGGGTGAAGAACGAGCTGGCCGCTCCGGACAGAATTTG; 314
Query 300 TCCGGACCATGTCACATGAGCGAGTGTCAAGATCATCCGGCCCGCTGCGCTG; 359
Db 366 ACCCAAGCAGCAGCCCTCTGCTGCTGAGGAGGAGGAGGAGGAGGAGG; 425
Query 420 CCATGGGAGATCTAGGAGCAGGAGAAAGGAGGAGGAGGAGGAGGAGG; 479
Db 486 CCTCCAGGAAACCTGGCTCTGAGCCAGTAGGGGCTGGCTGGAGGAGGAGG; 545
Query 540 GGGCCGGTAGGCTGCAAGAGAGCTCTGTTCCGAAGCTGAGCTGCTTACCG; 599
Db 546 GGGCCGGTAGGCTGCAAGAGAGCTCTGTTCCGAAGCTGAGCTGCTTACCG; 605
Query 600 TGGGGCTGGCAGGATGCCCCCTAGTCAGGG3A; 640
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RESULT 7

PCT-US01-18569-361
; Sequence 361, Application PCT/US01/18569

; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.

; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA13.PCT
; CURRENT APPLICATION NUMBER: PCT/US01/18569
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 361
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo sapiens
; PCT-US01-18569-361

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Query Match 98.0%; Score 627.4; DB 2; Length 1000;
Best Local Similarity 99.7%; Pred. No. 3.4e-107;
Matches 639; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
Query 1 CTCGGCGAGCGAGCGCGCTGCTAGCGCGAGCGCCCTGAGCGAGCGC; 60
Db 6 CTCCCGAGCGAGCGCGCTGCTAGCGCGAGCGCCCTGAGCGAGCGC; 65
Query 61 GGAG-GCCCGAGGCCCAACCGAGACACATCCCGCCGCCAGAGCCGGCTGCG; 119
Db 66 GGACCGCCAGGCCCAACCGAGACACATCCCGCCGCCAGAGCCGGCTGCG; 125
Query 120 CGCCAGCCGGCCCGCGATGCCCTACACGGCTTCAAGAGCGGAGCTCG; 179
Db 186 CGACCGCTGTAAGAGGATAGCAGCATGAGCTGGCCGCTCCGGACAGAATTTG; 245
Query 240 TCATGGAGCTACAGGGTGAAGAACGAGCTGGCCGCTCCGGACAGAATTTG; 299
Db 246 TCATGGAGCTACAGGGTGAAGAACGAGCTGGCCGCTCCGGACAGAATTTG; 314
Query 300 TCCGGACCATGTCACATGAGCGAGTGTCAAGATCATCCGGCCCGCTGCGCTG; 359
Db 366 ACCCAAGCAGCAGCCCTCTGCTGCTGAGGAGGAGGAGGAGGAGGAGG; 425
Query 420 CCATGGGAGATCTAGGAGCAGGAGAAAGGAGGAGGAGGAGGAGGAGG; 479
Db 486 CCTCCAGGAAACCTGGCTCTGAGCCAGTAGGGGCTGGCTGGAGGAGGAGG; 545
Query 540 GGGCCGGTAGGCTGCAAGAGAGCTCTGTTCCGAAGCTGAGCTGCTTACCG; 599
Db 546 GGGCCGGTAGGCTGCAAGAGAGCTCTGTTCCGAAGCTGAGCTGCTTACCG; 605
Query 600 TGGGGCTGGCAGGATGCCCCCTAGTCAGGG3A; 640
Db 606 TGGGGCTGGCAGGATGCCCCCTAGTCAGGG3A; 655

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QY 85 GGAGCCCCGGAGCCCCAAAACGGAGACACATCCCCGGCCCGAGGCCGCGCTCG 144
Db 120 CGCCCGGGGGCGCGCATGCCCTAGACCGGGGAGCTCG 179
QY 145 CGCCGAGCGGGCCGGGATGCCCTAGACCGGGCTTCAGAGCGGGAGCTCG 204
Db 180 CCCACCGCTGTAAGGAGGATACAGATCGGAGCACACCCAGCAAAATCCGGTA 239
QY 205 CCGACCGCTGTAAGGAGGATACAGATCGGAGCACACCCAGCAAAATCCGGTA 264
Db 240 TCATCAGGGCTACAGGTAGAGCAGCTGCCGAGCACACCCAGCAAAATCCGGTA 299
QY 265 TCATCAGGGCTACAGGTAGAGCAGCTGCCGAGCACACCCAGCAAAATCCGGTA 324
Db 300 TCCGGGACCATGTCACATGAGGGTGAAGATCATCCGGCCCTGGAGCTGA 359
QY 325 TCCGGGACCATGTCACATGAGGGTGAAGATCATCCGGCCCTGGAGCTGA 384
Db 360 ACCCACCGGGCTTCCTCGCTCGCTGAGCTATATGGCTACCG 419
QY 385 ACCCACCGGGCTTCCTCGCTCGCTGAGCTATATGGCTACCG 444
Db 420 CCATCGGGACATCTACGAGCAGGAAAGACGGAGCAGCACATGGTGAAGTGTGACCG 479
QY 445 CCATCGGGACATCTACGAGCAGGAAAGACGGAGCAGCACATGGTGAAGTGTGACCG 504
Db 480 CCTCCAGGAACCTTCGCTCTGAGCCAGTAGGGGGCTGGAGTCGG 539
QY 505 CCTCCAGGAACCTTCGCTCTGAGCCAGTAGGGGGCTGGAGTCGG 564
Db 540 GSCCCCGGTAGGCCCTGCCAGAGACCTCTGGTCTGAAGCTGAGCTGCCCTACCG 599
QY 565 GGCCTCCGGTACGCCCTGCCAGAGACCTCTGGTCTGAAGCTGAGCTGCCCTACCG 624
QY 600 TGGTGGCTGGGAGGATGTGCCCTAGTAGAGGGCA 640
Db 625 TGGTGGCTGGCAGCATGTGCCCTAGTAGAGGGCA 665

RESULT 12
US-09-428-151A-9451
: Sequence 941, Application US/09428151A
: GENERAL INFORMATION:
  APPLICANT: Glucksmann, M. Alexandra
  TITLE OF INVENTION: Nucleic Acid Molecules Derived from 'a
  FILE REFERENCE: 1600.1003001
  CURRENT APPLICATION NUMBER: US/09/428,151A
  CURRENT FILING DATE: 1999-10-27
  PRIOR APPLICATION NUMBER: 60/106,057
  PRIOR FILING DATE: 1998-10-28
  NUMBER OF SEQ ID NOS: 11036
  SOFTWARE: FastSEQ for Windows Version 3.0
  SEQ ID NO: 941
  LENGTH: 1356
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-09-428-151A-9451

Query Match 98 %; Score 627; DB 21; Length 1356;
Best Local Similarity 99.7%; Pred. No. 3.4e-107; Indels 1; Gaps 1;
Matches 639; Conservative 0; Mismatches 1; Gaps 1;

QY 1 CTCCCCGGAGCCGAGCCGCGCTACCGCGAGCCCGGAGCCCTTQAGCGGAGGGGC 60
Db 391 CTCCCCGGAGCCGAGCCGCGCTACCGCGAGCCCGGAGCCCTTQAGCGGAGGGGC 450
QY 61 GGAG-ACCGGAGCCCAACCGCAGACATCCCGGGCCAGAGCCCGGCCTGG 119
Db 451 GGAGCCCGGGAGCCCAACCGCAGACATCCCGGGCCAGAGCCCGGCCTGG 510
QY 120 CGCCAGCGGGCCGGCGCATGCCCTAGCGGCCCTTCAAGCGGGAGGTTG 179
Db 126 CGCCAGCGGGCCGGCGCATGCCCTAGCGGCCCTTCAAGCGGGAGGTTG 185
QY 179 CGCCAGCGGGCCGGCGCATGCCCTAGCGGCCCTTCAAGCGGGAGGTTG 239

RESULT 13
PCT-US98-15949-94
: Sequence 94, Application PC/US9815949
: GENERAL INFORMATION:
  APPLICANT: Human Genome Sciences, Inc., et al.
  TITLE OF INVENTION: 83 Human Secreted Proteins
  FILE REFERENCE: P2012PCT
  CURRENT APPLICATION NUMBER: PCT/US98/15949
  CURRENT FILING DATE: 1998-07-29
  NUMBER OF SEQ ID NOS: 219
  SOFTWARE: Patentin Ver. 2.0
  SEQ ID NO: 94
  LENGTH: 951
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE: SITE
: NAME/KEY: SITE
: LOCATION: (826)
: OTHER INFORMATION: n equals a,t,g, or c
: PCT-US98-15949-94

Query Match 98 %; Score 627; DB 1; Length 951;
Best Local Similarity 99.5%; Pred. No. 4.1e-107; Indels 1; Gaps 1;
Matches 638; Conservative 1; Mismatches 1; Gaps 1;

QY 1 CTCCCGCAGCGCCAGCCGCGCTGCTCAGCGGAGGCCCGGGCCCTTGGAGGGCG 60
Db 6 CTCCCCGGAGCCGAGCCGCGCTGCTCAGCGGAGGCCCGGGCCCTTGGAGGGCG 60
QY 61 GGAG-CCCCGGAGCCCAACCGCAGACATCCCGGGCCAGAGCCCGGCCTGG 119
Db 66 GGAGCCCGGGAGCCCAACCGCAGACATCCCGGGCCAGAGCCCGGCCTGG 125
QY 120 CGCCAGCGGGCCGGCGCATGCCCTAGCGGCCCTTCAAGCGGGAGGTTG 179
Db 126 CGCCAGCGGGCCGGCGCATGCCCTAGCGGCCCTTCAAGCGGGAGGTTG 185
QY 180 CGACCGCTGAGGGAGTACAGAGATCGGGGACCGAGCCCCAGCAAAATCCGGTA 239
Db 631 TCATCAGGGCTACAGGTAGAGCAGCTGCCGAGCACACCCAGCAAAATCCGGTA 690
Db 751 CGACCGCTGAGGGAGTACAGAGATCGGGAGCACACCCAGCAAAATCCGGTA 630
Db 751 TCATCAGGGCTACAGGTAGAGCAGCTGCCGAGCACACCCAGCAAAATCCGGTA 630
Db 420 CCATCGGGACATCTACGAGCAGGAGAAGACGGAGCAGCACATGGTGAAGTGTGACCG 479
QY 811 CCATCGGGACATCTACGAGCAGGAGAAGACGGAGCAGCACATGGTGAAGTGTGACCG 810
Db 871 CCTCCAGGAACCTTCGGCTCTGAGCAGCTGAGCTGGGGCTCGGCTCGGCTCGGG 930
Db 931 GGGCCCGGTCAGGCCCTGCCAGAGAGCTCTGTTCTGAAGTGTGAGCTGCCCTACCG 990
QY 600 TGGTGGCTGGCAGGATGTGCCCTAGTAGAGGGCA 640
Db 991 TGGTGGCTGGCAGGATGTGCCCTAGTAGAGGGCA 1031

RESULT 14
Db 511 CGCCAGCGGGCCGGCGATGCCCTCAGCGGGCTTCAGCGGGAGCTCG 570
QY 180 CGACCGCTGAGGGAGTACAGAGATCGGGGACCGAGCCCCAGCAAAATCCGGTA 239
Db 571 CGACCGCTGAGGGAGTACAGAGATCGGGAGCACACCCAGCAAAATCCGGTA 630
Db 240 TCATCAGGGCTACAGGTAGAGCAGCTGCCGAGCACACCCAGCAAAATCCGGTA 299
Db 691 TCCTGGGACCATGTCACATGAGGGTGAAGATCATCCGGCGCGCTGAGCTGA 750
Db 360 ACCCCAGGAGCCCTTCCTGCTGTAAGCATGCCGAGCACAGCATGGTGAAGTGTGACCG 419
Db 751 ACCCCAGGAGCCCTTCCTGCTGTAAGCATGCCGAGCACAGCATGGTGAAGTGTGACCG 810
Db 420 CCATCGGGACATCTACGAGCAGGAGAAGACGGAGCAGCACATGGTGAAGTGTGACCG 479
QY 811 CCATCGGGACATCTACGAGCAGGAGAAGACGGAGCAGCACATGGTGAAGTGTGACCG 810
Db 871 CCTCCAGGAACCTTCGGCTCTGAGCAGCTGAGCTGGGGCTCGGCTCGGCTCGGG 930
Db 931 GGGCCCGGTCAGGCCCTGCCAGAGAGCTCTGTTCTGAAGTGTGAGCTGCCCTACCG 990
QY 540 GGGCCCGGTCAGGCCCTGCCAGAGACCTCTGGCTCTGAGCAGCTGAGCTGCCCTACCG 599
Db 991 TGGTGGCTGGCAGGATGTGCCCTAGTAGAGGGCA 1031

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Db 186 CGGACCGCTGTAGGGAGTACAGAGATOCGGACAGACCCAGCAAAATCCGGTA 245
QY 240 TCACTGAGGCGCTACAGGGTAGAGAGCTGCGCTCTGGACAAGAGTAAAGTTTGG 299
Db 246 TCACTGAGGCGCTACAGGGTAGAGAGCTGCGCTCTGGACAAGAGTAAAGTTTGG 305
Db 300 TCCGGACCATGTCACATGAGGACTGGTCAAGATCATCGGGGCGCGCTGAGCTGA 359
Db 305 TCCGGACCATGTCACATGAGGAGTGGTCAAGATCATCGGGGCGCGCTGAGCTGA 365
Db 360 ACCCGAGCGAGCTCTCCGCTGGTGAACCCAGCACAGCATGGTGAATGTCACCC 419
Db 366 ACCCGAGCGAGCTCTCCGCTGGTGAACCCAGCACAGCATGGTGAATGTCACCC 425
Db 420 CCATCGGAGACATCTACGAGCAGAGAAGAGACGAGGAGCTCCTATAGTCTACCG 479
Db 426 CCATCGGAGACATCTACGAGCAGAGAAGAGACGAGGAGCTCCTATAGTCTACCG 485
Db 480 CTCGCCAGGAACCTCGCTCTGACCGAGTATGGGGCTGGGAGTCGG 539
Db 486 CCCTCCAGGAACCTCTGCGCTCTGAGGCCAGTATGGGGCTGGGAGTCGG 545
QY 540 GGGCCCTGGCTAGGCCCTGCCAGAGACTCTGACTTCTGACTTCTCTCTACGG 599
Db 546 GGGCCCTGGCTAGGCCCTGCCAGAGACTCTGACTTCTGACTTCTCTCTACGG 605
Db 600 TGGTGGCTGGAGGAGTGTGCCCCCTAGTCAGAGGCA 640
Db 606 TGGTGGCTGGAGGAGTGTGCCCCCTAGTCAGAGGCA 646
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RESULT 14
PCT-US98-15949-94
; Sequence 94, Application PCT/US9815949
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc., et al.
; TITLE OF INVENTION: 83 Human Secreted Proteins
; FILE REFERENCE: P2012PCT
; CURRENT APPLICATION NUMBER: PCT/US98/15949
; CURRENT FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 219
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 94
; LENGTH: 951
; TYPE: lNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (826)
; OTHER INFORMATION: n equals a, t, g, or c
; PCT-US98-15949-94

Query Match 98.0% Score 627; DB 2; Length 951;
Best Local Similarity 99.5%; Pred. No. 4; 1e-107; Matches 638; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
US-60-172-373-10400

RESULT 15
US-60-172-373-10400
; Sequence 10400, Application US/60172-74
; GENERAL INFORMATION:
; APPLICANT: Morris, McDonald
; APPLICANT: Dier, Dinh
; APPLICANT: Morris, Preeti
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; FILE REFERENCE: GR-0006_P
; CURRENT APPLICATION NUMBER: US/60-172, 74
; CURRENT FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 25,772
; SOFTWARE: PERL program
; SEQ ID NO: 10400
; LENGTH: 1017
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; OTHER INFORMATION: Incept. ID No.: 247776, 3
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 4, 25, 46
; OTHER INFORMATION: a, t, c, g, or other
; OTHER INFORMATION: a, t, c, g, or other
US-60-172-373-10400

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Best Local Similarity 99.4%; Pred. No. 4; 3e-103; Matches 639; Conservative 0; Mismatches 1; Indels 3; Gaps 4;
Db 61 GAG-G-CGGAGGCCCAACGCCAGACACATCCGCGCCAGAGCGCGCTCG 119
Db 66 GGAGCCCGGGAGCCCAACCGAGACACATCCGCGCCAGAGCGCGCTCG 125
Db 120 GGGCCAGCGGCCGGCGATGCCCTAGACGGCGCTTCAGAGAAGGGCGAGCTGG 179
Db 126 CGCCGAGCGGCCGGCGATGCCCTAGACGGCGCTTCAGAGAAGGGCGAGCTGG 185
Db 180 CGGACCGCTGTAGGGTGTACACAGATCCGCGACCAAGCCAGAAATCCGGTA 239,
Db 186 CGGACCGCTGTAGGGTGTACACAGATCCGCGACCAAGCCAGAAATCCGGTA 245
Db 240 TCACTGAGGCGCTACAGGGTAGAGAGCTGCGCTCTGGACAAGAGTAAAGTTG 299
Db 246 TCACTGAGGCGCTACAGGGTAGAGAGCTGCGCTCTGGACAAGAGTAAAGTTG 305
Db 300 TCCGGACCATGTCACATGAGGACTGGTCAAGATCATCGGGGCGCGCTGAGCTGA 359
Db 305 TCCGGACCATGTCACATGAGGAGTGGTCAAGATCATCGGGGCGCGCTGAGCTGA 365
Db 360 ACCCGAGCGAGCTCTCCGCTGGTGAACCCAGCACAGCATGGTGAATGTCACCC 419
Db 366 ACCCGAGCGAGCTCTCCGCTGGTGAACCCAGCACAGCATGGTGAATGTCACCC 425
Db 420 CCATCGGAGACATCTACGAGCAGAGAAGAGACGAGGAGCTCCTATAGTCTACCG 479
Db 426 CCATCGGAGACATCTACGAGCAGAGAAGAGACGAGGAGCTCCTATAGTCTACCG 485
Db 480 CTCGCCAGGAACCTCGCTCTGACCGAGTATGGGGCTGGGAGTCGG 539
Db 486 CCCTCCAGGAACCTCTGCGCTCTGAGGCCAGTATGGGGCTGGGAGTCGG 545
QY 540 GGGCCCTGGCTAGGCCCTGCCAGAGACTCTGACTTCTGACTTCTCTCTACGG 599
Db 546 GGGCCCTGGCTAGGCCCTGCCAGAGACTCTGACTTCTGACTTCTCTCTACGG 605
Db 600 TGGTGGCTGGAGGAGTGTGCCCCCTAGTCAGAGGCA 640
Db 606 TGGTGGCTGGAGGAGTGTGCCCCCTAGTCAGAGGCA 646
Db 606 TGGTGGCTGGAGGAGTGTGCCCCCTAGTCAGAGGCA 646

RESULT 16
US-60-172-373-10400
; Sequence 10400, Application US/60172-74
; GENERAL INFORMATION:
; APPLICANT: Morris, McDonald
; APPLICANT: Dier, Dinh
; APPLICANT: Morris, Preeti
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; FILE REFERENCE: GR-0006_P
; CURRENT APPLICATION NUMBER: US/60-172, 74
; CURRENT FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 25,772
; SOFTWARE: PERL program
; SEQ ID NO: 10400
; LENGTH: 1017
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; OTHER INFORMATION: Incept. ID No.: 247776, 3
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 4, 25, 46
; OTHER INFORMATION: a, t, c, g, or other
; OTHER INFORMATION: a, t, c, g, or other
US-60-172-373-10400

Query Match 94.6% Score 605; DB 71; Length 1017;
Best Local Similarity 99.4%; Pred. No. 4; 3e-103; Matches 639; Conservative 0; Mismatches 1; Indels 3; Gaps 4;
Db 71 CGCCGAGCGGCCAGCGCGCTGGTCAAGAGAAGGGCGCGCTGAGCTGG 149
Db 71 CGCCGAGCGGCCAGCGCGCTGGTCAAGAGAAGGGCGCGCTGAGCTGG 149
QY 71 CGCCGAGCGGCCAGCGCGCTGGTCAAGAGAAGGGCGCGCTGAGCTGG 149
Db 61 GAG-G-CGGAGGCCCAACGCCAGACACATCCGCGCCAGAGCGCGCTCG 117
Db 131 GAG-G-CGGAGGCCCAACGCCAGACACATCCGCGCCAGAGCGCGCTCG 190
Db 131 GAG-G-CGGAGGCCCAACGCCAGACACATCCGCGCCAGAGCGCGCTCG 190
Db 188 CGGACCGCTGTAGGGTGTACACAGATCCGCGACCAAGCCAGAAATCCGGTA 239,
Db 191 CGGACCGCTGTAGGGTGTACACAGATCCGCGACCAAGCCAGAAATCCGGTA 245
Db 240 TCACTGAGGCGCTACAGGGTAGAGAGCTGCGCTCTGGACAAGAGTAAAGTTG 299
Db 246 TCACTGAGGCGCTACAGGGTAGAGAGCTGCGCTCTGGACAAGAGTAAAGTTG 305
Db 300 TCCGGACCATGTCACATGAGGACTGGTCAAGATCATCGGGGCGCGCTGAGCTGA 359
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Db 360 ACCCGAGCGAGCTCTCCGCTGGTGAACCCAGCACAGCATGGTGAATGTCACCC 419
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QY 540 GGGCCCTGGCTAGGCCCTGCCAGAGACTCTGACTTCTGACTTCTCTCTACGG 599
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Search completed: August 15, 2003, 10:21:12  
Job time : 2938 secs

GenScore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

August 11, 2003, 09:49:08 ; Search time 83 Seconds

(without alignments) 231.397 Million cell updates/sec

Title: OS-09-904-603-1

Perfect score: 625

Sequence: 1 MPSDRFFKQRRSFADRCKEV..... EKDEDGFLYVWYASQETFGF 121

Scoring table: BLOSUM2

Gapop 10.0 , Gapext 0.5

Searched:

1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters:

1107863

Minimum DH seq length: 0

Maximum DH seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /SIDS1/qcadata/qeneseq/geneseq-emb1/AA1982.DAT;\*

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16: /SIDS1/qcadata/qeneseq/geneseq-emb1/AA1995.DAT;\*

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18: /SIDS1/qcadata/qeneseq/geneseq-emb1/AA1997.DAT;\*

19: /SIDS1/qcadata/qeneseq/geneseq-emb1/AA1998.DAT;\*

20: /SIDS1/qcadata/qeneseq/geneseq-emb1/AA1999.DAT;\*

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22: /SIDS1/qcadata/qeneseq/geneseq-emb1/AA2001.DAT;\*

23: /SIDS1/qcadata/qeneseq/geneseq-emb1/AA2002.DAT;\*

24: /SIDS1/qcadata/qeneseq/geneseq-emb1/AA2003.DAT;\*

### RESULT 1

ID AA069979  
ID AA069979 standard: Protein; 121 AA.

XX AA069979;

XX AC

XX DT

20-NOV-1998 (first entry)

XX DE

XX Human microtubule associated protein hLc3.

XX KW

XX Human; microtubule-associated protein; hMAP; cell proliferation; cancer.

XX OS

OS Homo sapiens.

XX PN

XX WO9837197-A1.

XX PD

27-AUG-1998.

XX PF

23-FEB-1998;

98W1-1804744.

XX PR

24-FEB-1997;

97US-1805117.

XX PA

(INCYT) INCYTE PHARM INC.

XX PI

Goil SK, Hilman JL;

XX DR

WPI; 1998-467560/40.

XX DR

N-PSDB; AAV43780.

XX PT

New isolated human microtubule-associated protein - used to develop PT products for use in the diagnosis, prevention and treatment of disorders associated with cell proliferation, particularly cancer.

Pre. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARES

Result No.	Score	Query Match Length	DB ID	Description
1	625	100.0	121 19	AAW69979 Human microtubule
2	625	100.0	159 23	Human ovarian anti
3	625	100.0	199 22	ABG09793 Novel human dipeptid
4	625	83.4	125 22	Human Mpi3 protein
5	621	83.4	125 22	ABG74775 Human tumour suppr
6	621	83.4	125 23	ABG19539 Human secretory po
7	621	83.4	130 23	Rat Mpi3 protein
8	521	83.4	142 22	ABG74776 Human polypeptide
9	521	83.4	155 22	AAW41446

XX  
PS Claim 1; Fig 1; 58pp; English.  
XX  
CC Human microtubule-associated protein (hMAP) expression is associated with  
CC disorders of cell proliferation, in particular, cancer. The hMAP and  
CC agonists can be used to stimulate cell proliferation. Tissues or  
CC organs generated by these methods may be introduced or transplanted into  
CC a subject for the purpose of treating a variety of diseases. Antagonists  
CC or inhibitors of hMAP can be used to treat or prevent disorders  
CC associated with cell proliferation, particularly cancers. The products  
CC can also be used for detection, diagnosis and drug screening.  
XX  
SQ Sequence 121 AA;  
Query Match 100.0%; Score 625; DB 19; Length 121;  
Best Local Similarity 100.0%; Pred. No. 4.9e-65;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 MPSDRPKKQRSFADRCKEVOQIRDQHPSKIPVIERYKEQKOLPVLDTKFLVPHVM 60  
1 MPSDRPKKQRSFADRCKEVOQIRDQHPSKIPVIERYKEQKOLPVLDTKFLVPHVM 60  
QY 61 SELVKIRRQLQNLNPTQAFELLVNVNQHSMWSVSTPIADIYEQEKEQEDGFLYMWVQASQETFG 120  
Db 61 SELVKIRRQLQNLNPTQAFELLVNVNQHSMWSVSTPIADIYEQEKEQEDGFLYMWVQASQETFG 120  
QY 121 F 121  
Db 121 F 121  
RESULT 2  
ABP41404  
ID ABP41404 standard; Protein; 169 AA.  
XX  
AC ABP4140M;  
XX DT 22-AUG-2002 (first entry)  
XX DE Human ovarian antigen HRATL31, SEQ ID NO:2536.  
XX Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;  
KW ovarian cancer; breast cancer; tumour; reproductive system disorder;  
KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;  
KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;  
KW inflammatory condition; immune disorder; blood disorder;  
KW cardiovascular disorder; respiratory disorder; neurological disorder;  
KW gastrointestinal disorder; urinary system disorder; drug screening;  
KW gene therapy; chromosome mapping; forensic analysis;  
KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;  
KW antiinflammatory; gynaecological; reproductive.  
OS Homo sapiens.  
XX WO200200677-A1.  
XX 03-JAN-2002.  
XX 07-JUN-2001; 2001WO-US18569.  
XX PR 07-JUN-2000; 2000US-209467P.  
XX (HUMA-) HUMAN GENOME SCI INC.  
PT Birse CE, Rosen CA;  
XX DR WPI; 2002-147878/19.  
DR N-PSDB; AB054481.  
XX Isolated nucleic acid molecules encoding novel ovarian polypeptides,  
PT useful in the prevention, treatment and diagnosis of cancer (e.g.  
PT ovarian cancer), immune disorders, cardiovascular disorders and  
PT neurological diseases -

XX  
PS Claim 11; SEQ ID NO 2536; 2922PP; English.  
XX  
CC The invention relates to 2175 novel human ovarian antigens (ABP41054-  
CC ABP413228) and to cDNAs encoding them (AB05131-AB05605), and also  
CC encompasses polyptides 90% identical and polynucleotides 95% identical  
CC to the sequences of the invention. The invention additionally relates to  
CC recombinant vectors and host cells comprising human ovarian antigen  
CC of ovarian antigen polynucleotides and polyptides in diagnosing,  
CC treating, prognosis or preventing various ovary and/or breast-related  
CC disorders. Such conditions include ovarian cancer and breast cancer, and  
CC metastatic tumours of ovarian or breast origin, reproductive system  
CC disorders (e.g., infertility, disorders of pregnancy, anovulation,  
CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine  
CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic  
CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and  
CC vaginitis), immune disorders (e.g., congenital and acquired  
CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),  
CC blood-related disorders (e.g., anaemia), cardiovascular disorders,  
CC respiratory disorders, neurological disorders, gastrointestinal disorders  
CC and urinary system disorders. Ovarian antigen polyptides and  
CC polyrnucleotides may also be used in screening for compounds which may  
CC further be used for gene therapy, chromosome mapping, in the  
CC identification of individuals and in forensic analysis, and the  
CC polypeptides may be used as food additives or to prepare antibodies  
CC useful in disease diagnosis, drug targeting and phenotyping. The present  
CC sequence represents a human ovarian antigen of the invention.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at [ftp://wipo.int/pub/published\\_pct\\_sequences](ftp://wipo.int/pub/published_pct_sequences).  
XX  
SQ Sequence 169 AA;  
Query Match 100.0%; Score 625; DB 23; Length 169;  
Best Local Similarity 100.0%; Pred. No. 7.6e-65;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MPSDRPKKQRSFADRCKEVOQIRDQHPSKIPVIERYKEQKOLPVLDTKFLVPHVM 60  
Db 49 MPSDRPKKQRSFADRCKEVOQIRDQHPSKIPVIERYKEQKOLPVLDTKFLVPHVM 108  
QY 61 SELVKIRRQLQNLNPTQAFELLVNVNQHSMWSVSTPIADIYEQEKEQEDGFLYMWVQASQETFG 120  
Db 109 SELVKIRRQLQNLNPTQAFELLVNVNQHSMWSVSTPIADIYEQEKEQEDGFLYMWVQASQETFG 168  
QY 121 F 121  
Db 169 F 169  
RESULT 3  
ID ABG09793  
ID ABG09793 standard; Protein; 199 AA.  
XX AC ABG09793;  
XX DT 13-FEB-2002 (first entry)  
XX Novel human diagnostic protein #9784.  
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;  
XX food supplement; medical imaging; diagnostic; genetic disorder.  
OS Homo sapiens.  
XX WO200175067-A2.  
XX 11-OCT-2001.  
XX 30-MAR-2001; 2001WO-US08631.

PR	31-MAR-2000; 2000US-0540217.	KW	Leukaemia.
PR	23-AUG-2000; 2000US-0649167.	XX	
XX		OS	Homo sapiens.
PA	(HYSEQ-)	XX	
XX		PN	WO200153312-A1.
PI	Dimanac RT, Liu C, Tang YT;	XX	
XX		PD	26-JUL-2001.
DR	WPI; 2001-639362/73.	XX	
XX	N-PSDB; AAS73980.	PF	26-DEC-2000; 2000WO-US34263.
PT	New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity	XX	
PT	for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II), to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and (II) are useful for treating imaging of sites expressing (II). (I) and (II) are useful in medical disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.	XX	
CC	Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at <a href="http://wipo.int/pub/published_pct_sequences">ftp://wipo.int/pub/published_pct_sequences</a> .	XX	
CC	Sequence 199 AA:	XX	
Query	Match 100.0%; Score 625; DB 22; Length 199; Best Local Similarity 100.0%; Pred. No. 9.4e-65; Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	XX	
QY	1 MPSDRPFKQRRSFADRKCKEVQOIRDQHPSKIPVITERYKGKEKLPVLDKTKFLVDPDHNM 60	XX	
Db	52 MPSDRPFKQRRSFADRKCKEVQOIRDQHPSKIPVITERYKGKEKLPVLDKTKFLVDPDHNM 111	XX	
QY	61 SELVKIRRRLQNLNPTQAFFLNVQHSMVSVSTPIADIYEQEKEDEGFLYMVVASQETFG 120	XX	
Db	112 SELVKIRRRLQNLNPTQAFFLNVQHSMVSVSTPIADIYEQEKEDEGFLYMVVASQETFG 171	XX	
QY	121 F 121	XX	
Db	172 F 172	XX	
Query	Match 83.4%; Score 521; UB 22; Length 125; Best Local Similarity 82.5%; Pred. No. 7.2e-53; Matches 99; Conservative 12; Mismatches 9; Indels 0; Gaps 0;	XX	
QY	1 MPSDRPFKQRRSFADRKCKEVQOIRDQHPSKIPVITERYKGKEKLPVLDKTKFLVDPDHNM 60	XX	
Db	1 MPSDRPFKQRRSFADRKCKEVQOIRDQHPSKIPVITERYKGKEKLPVLDKTKFLVDPDHNM 60	XX	
RESULT 4		XX	
ID	AAM39660	XX	
ID	AAM39660 standard; Protein: 125 AA.	XX	
AC	AAM39660;	XX	
DT	22-OCT-2001 (first entry)	XX	
DE	Human polypeptide SEQ ID NO 2805.	XX	
KW	Human; notropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;	XX	







Db 47 MPSEKTFKQRTFEQRVEDVRLIREQHPTKIPVIERVKGEKOLPVLDKTKFLVDPDHNM 106 Qy 24 RDQHPSKIPVILERYKGKQIPWLDKTKFLVDPDHNMSELVKIRRLQJINPQIAPPV 114  
 Qy 61 SELVKIRRLQNPQTOAFFLIVNQHSAVSVTPIADIYEOKDEDGLYMYA-SQETFG 120 Db 1 RDQHPSKIPVILERYKGKQIPWLDKTKFLVDPDHNMSELVKIRRLQJINPQIAPPV 114  
 Db 107 SELKIKRRLQLNQAFFLVLVNGHSAVSVTPISEVESEKDEDGLYMYA-SQETFG 166 Qy 84 NOHSMVSVSTPIADIYEQEKEDEGSFLYMYGLPCKPFGF 99  
 RESULT 11  
 ABG0974  
 ID ABG0974 standard; Protein: 99 AA.  
 XX AC ARG0974;  
 XX AC ARG0974;  
 XX DT 14-FEB-2002 (first entry)  
 XX DE Novel human diagnostic protein #9785.  
 XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.  
 XX OS Homo sapiens.  
 XX PN W1200175067-A2.  
 XX PD 11-OCT-2001.  
 XX PF 30-MAR-2001; 2001WO-US08631.  
 XX PR 31-MAR-2000; 2000US-0540217.  
 XX PR 24-AUG-2000; 2000US-0649167.  
 XX PA (HYSE-) HYSEQ INC.  
 XX PI Demanac RT, Liu C, Tang YT;  
 XX DR WPI; 2001-639362/73.  
 DR N-PSDB: AAST3981.  
 XX PT New isolated polynucleotide and encoded polypeptides, useful in PT diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess PT biodiversity.  
 XX PS Claim 20; SEQ ID No 40153; 103pp; English.  
 XX PS  
 XX The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG0010-ABG3037 represent novel human diagnostic amino acid sequences of the invention.  
 Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at <http://wipo.int/pdb/published-pct-sequences>.  
 XX SO Sequence 99 AA;  
 XX Sequence, 99 AA;  
 Query Match 74.6%; Score 466.5; DB 22; Length 99;  
 Best Local Similarity 93.9%; Pred. No. 1.2e-46;  
 Matches 33; Conservative 1; Mismatches 4; Indels 1; Caps 1;  
 Query Match 1 MPSURPKKRSKPAKQWVJRDWHSKPI-WIERYKGKQIPWLDKTKFLVDPDHNM 59 Db 32 MPSEKTFKQRTFEQRVEDVRLIREQHPTKIPVIERVKGEKOLPVLDKTKFLVDPDHNM 91

RESULT 12  
 AAU30602  
 ID AAU30602 standard; Protein: 222 AA.  
 XX AC AAU30602;  
 XX DT 18-DEC-2001 (first entry)  
 XX DE Novel human secreted protein #1043.  
 XX KW Human; vaccination; gene therapy; nutritional supplement; stem cell proliferation; haematopoiesis; nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaemia.  
 XX OS Homo sapiens.  
 XX PN WO200179449-A2.  
 XX PD 25-OCT-2001.  
 XX PR 16-APR-2001; 2001W1-US08655f.  
 XX PR 18-APR-2000; 2000US-0552929.  
 XX PR 26-JAN-2001; 2001US-0770160.  
 XX PA (HYSE-) HYSEQ INC.  
 XX PI Tang YT, Liu C, Demanac RT;  
 XX DR WPI; 2001-611725770.  
 XX PT Nucleic acids encoding a range of human polypeptides, useful in diagnostic vaccination, testing and therapy - PT  
 XX PS Claim 20; Page 316; 765pp; English.  
 XX CC The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression of physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haemopoiesis, and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAU29510-AAU3304 represent the amino acid sequences of novel human secreted proteins of the invention.  
 XX SO Sequence 222 AA;  
 XX Sequence, 222 AA;  
 Best Local Similarity 67.2%; Pred. No. 1.1e-39;  
 Matches 82; Conservative 16; Mismatches 22; Indels 2; Caps 2;  
 Query Match 1 MPSURPKKRSKPAKQWVJRDWHSKPI-WIERYKGKQIPWLDKTKFLVDPDHNM 59 Db 32 MPSEKTFKQRTFEQRVEDVRLIREQHPTKIPVIERVKGEKOLPVLDKTKFLVDPDHNM 91



CC e.g. stem cell growth factor activity, haematopoiesis regulating  
 CC activity, tissue growth factor activity, immunomodulatory activity and  
 CC antiinhibin activity and may be useful in the diagnosis and/or  
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and  
 CC inflammation.  
 CC Note: records for SEQ ID NO 2110 (AK52581), 2111 (AK52582) and 3666  
 CC (AK52580) are omitted as the relevant pages from the sequence listing  
 CC were missing at the time of publication.

XX SQ Sequence 120 AA:  
 Query Match 48.2%; Score 301; DB 22; Length 120;  
 Best Local Similarity 59.28; Pred. No. 3.4e-27;  
 Matches 58; Conservative 16; Mismatches 24; Indels 0; Gaps 0;  
 QY 23 IRODHPSKPVITERYKQKQLPVLKDKEFLVPHVNMSCLVKIRRQLQNLPTQAFFL 82  
 Db 2 IRAKEPKNPKVWVYPRFLKFLVPOELTMFLSIRSRAWLAERAFYIL 61  
 QY 83 VNOHSMWSVSTPIADYFQEKEDGFLYMYASQETFG 120  
 Db 62 VNNKSLVMSATMAEYRDYKEDGFLYVWVYASQETFG 99

RESULT 15  
 ABG56031  
 ID ABG56031 standard: Peptide: 53 AA.  
 XX  
 AC AC  
 XX  
 DE Human liver peptide, SEQ ID No 34679.  
 XX  
 KW Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;  
 XX  
 KW hypercholesterolaemia; coronary heart disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2001157273-A2.  
 PD 09 AUG 2001.  
 XX  
 PR 30-JAN-2001; 2001WO-US00664.  
 XX  
 PR 04-FEB-2000; 2000US-0180312.  
 PR 26-MAY-2000; 2000US-0207456.  
 PR 30-JUN-2000; 2000US-0508408.  
 PR 01-AUG-2000; 2000US-0632366.  
 PR 21-SEP-2000; 2000US-0234667.  
 PR 27-SEP-2000; 2000US-0236359.  
 PR 04-OCT-2000; 2000GB-0024263.  
 XX  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX  
 P1 Peut S.; Hanzel DK.; Chen W.; Rank DR;  
 XX  
 DR WFT; 2001-488898/53.  
 XX  
 PT Human genome-derived single exon nucleic acid probes useful for  
 PT analysing gene expression in human adult liver -  
 XX  
 P5 Claim 27: SEQ ID No 34679; 658pp; English.

CC The invention relates to a single exon nucleic acid probe (SEN1P) (1) for  
 CC measuring human gene expression in a sample derived from human adult  
 CC liver, comprising one of 13109 defined nucleotide sequences given in the  
 CC specification (or complements/ fragments). The probe hybridises at high  
 CC stringency to a nucleic acid molecule expressed in the human adult  
 liver. (1) may be used for predicting, measuring and displaying gene  
 CC expression in samples derived from human adult liver. The genes  
 CC identified may be involved in genetic liver diseases such as cirrhosis,  
 CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which

CC is associated with coronary heart disease. ABG47348 ABG55930 represent  
 CC human liver single exon encoded peptides of the invention.  
 CC Note: The sequence information for this patent does not appear in the  
 CC printed specification but was obtained in electronic format directly  
 CC from WIPO at <http://wipo.int/put/published-pct/sequences>.

XX SQ Sequence 53 AA:  
 Query Match 43.5%; Score 272; DB 22; Length 54;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-24;  
 Matches 53; Conservative 10; Mismatches 0; Indels 0; Gaps 0;  
 QY 69 RRLQINPQIAFEFLVNVHSWWSVSI11A11YEQEKEDEFLYLYMYSAS21FNF 121  
 Db 1 RRLQINPQIAFEFLVNVHSWWSVSI1A11YEQEKEDEFLYLYMYSAS21FNF 53  
 Search completed: August 11, 2003, 10:13:14  
 Job time : 84 secs

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KLINIKEN

US-08-005-117-1  
Sequence 1, Application US/08805117  
PATENT NO. 5,953,122  
GENERAL INFORMATION:  
APPLICANT: Hillman, Jennifer L.  
APPLICANT: Goil, Surya K.  
TITLE OF INVENTION: NOVEL MICK-JUBILEE-ASSOCIATED PROTEIN  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/805,117  
FILING DATE: Herewith  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0211 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-845-0555  
TELEFAX: 415-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 121 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: THYROMIUS  
CLONE: 144378  
US-08-805-117-1

Query Match 100.0% Score 625; DB 2; Length 121;  
Best Local Similarity 100.0%; Fred. No. 2.2e-69;  
Matches 121; Conservative 0; Mismatches 0; Indels 0;

QY. 1 MPSDRFPKQRSFADRCKEVQIROQHPSKIPVILERYKEGKQLPVLDKTKFLVDPHNM 60  
 Db 1 MPSDRFPKQRSFADRCKEVQIROQHPSKIPVILERYKEGKQLPVLDKTKFLVDPHNM 60

QY. 61 SELVKIRRQLNPTQAFLLVNHSMVSVSTPIADIVQEKDEDGFLYMVYASQETFG 120  
 Db 61 SELVKIRRQLNPTQAFLLVNHSMVSVSTPIADIVQEKDEDGFLYMVYASQETFG 120

QY. 121 F 121  
 Db 121 F 121

RESULT 2  
 US-09-199-838-1  
 ; Sequence 1, Application US/09199838  
 ; Patent No. 6280733  
 GENERAL INFORMATION:  
 APPLICANT: Hillman, Jennifer L.  
 TITLE OF INVENTION: NOVEL MICROTUBULE-ASSOCIATED PROTEIN  
 NUMBER OF SEQUENCES: 3  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 STREET: 3174 Porter Drive  
 CITY: Palo Alto  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94304  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FASTSEQ for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/199, 838  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/805, 117  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Billings, Lucy J.  
 REGISTRATION NUMBER: 36,749  
 REFERENCE/DOCKET NUMBER: PP-0211 US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-855-0555  
 TELEFAX: 415-845-4166  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 121 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 IMMEDIATE SOURCE:  
 LIBRARY: Thyrnotropin  
 CLONE: 144378  
 ; US-09-199-838-1

Query Match 100.0%; Score 625; DB 3; Length 121;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-69;  
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY. 1 MPSDRFPKQRSFADRCKEVQIROQHPSKIPVILERYKEGKQLPVLDKTKFLVDPHNM 60  
 Db 1 MPSDRFPKQRSFADRCKEVQIROQHPSKIPVILERYKEGKQLPVLDKTKFLVDPHNM 60

QY. 61 SELVKIRRQLNPTQAFLLVNHSMVSVSTPIADIVQEKDEDGFLYMVYASQETFG 120  
 Db 61 SELVKIRRQLNPTQAFLLVNHSMVSVSTPIADIVQEKDEDGFLYMVYASQETFG 120

RESULT 3  
 US-08-805-117-3  
 ; Sequence 3, Application US/08805117  
 ; Patent No. 5955312  
 GENERAL INFORMATION:  
 APPLICANT: Hillman, Jennifer L.  
 APPLICANT: Gol, Surya K.  
 TITLE OF INVENTION: NOVEL MICROTUBULE-ASSOCIATED PROTEIN  
 NUMBER OF SEQUENCES: 3  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 STREET: 3174 Porter Drive  
 CITY: Palo Alto  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94304  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FASTSEQ for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/805, 117  
 FILING DATE: Herewith  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Billings, Lucy J.  
 REGISTRATION NUMBER: 36,749  
 REFERENCE/DOCKET NUMBER: PP-0211 US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-855-0555  
 TELEFAX: 415-845-4166  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 142 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 IMMEDIATE SOURCE:  
 LIBRARY: GenBank  
 CLONE: 455109  
 ; US-08-805-117-3

Query Match 83.4%; Score 521; DB 2; Length 142;  
 Best Local Similarity 82.5%; Pred. No. 1.7e-56;  
 Matches 99; Conservative 12; Mismatches 9; Indels 0; Gaps 0;

QY. 1 MPSDRFPKQRSFADRCKEVQIROQHPSKIPVILERYKEGKQLPVLDKTKFLVDPHNM 60  
 Db 1 MPSERFTKQRSFECRVEDVRLRQHPKVPIVILERYKEGKQLPVLDKTKFLVDPHNM 60

QY. 61 SELVKIRRQLNPTQAFLLVNHSMVSVSTPIADIVQEKDEDGFLYMVYASQETFG 120  
 Db 61 SELVKIRRQLNPTQAFLLVNHSMVSVSTPIADIVQEKDEDGFLYMVYASQETFG 120

RESULT 4  
 US-09-199-838-3  
 ; Sequence 3, Application US/09199838  
 ; Patent No. 6280733  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hillman, Jennifer L.  
 ; APPLICANT: Gol, Surya K.  
 ; TITLE OF INVENTION: NOVEL MICROTUBULE-ASSOCIATED PROTEIN



FILING DATE: 16-Aug-2001  
 CLASSIFICATION: <unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Meyers, Kenneth J.  
 REGISTRATION NUMBER: 25,146  
 REFERENCE/DOCKET NUMBER: 02356.0073-00000  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 408-0400  
 TELEFAX: (202) 408-4400  
 INFORMATION FOR SEQ ID NO: 9:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 724 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 MOLECULE DESCRIPTION: SEQ ID NO: 9:  
 US-08-671-57A-9

Query Match 12.4%; Score 77.5; DB 4; Length 724;  
 Best Local Similarity 21.8%; Pred. No. 0 62; Mismatches 42; Indels 1; Gaps 1;  
 Matches 19; Conservative 25; MisMatches 42; Indels 1; Gaps 1;

Qy 18 KEVOOIRDRHPSKIPVIERYKEQKIPVLDK-TKFLVDPDHVNMSLEVKKIRRLQLNPT 76  
 Db 533 QEVONLILDKVKNDYPLIVEGALGVAPVSLIQKILKDHIPKOMLTLIESVSDIAEV 592

Qy 77 QAFFLVLNQHSMWSVSPIDYEQEK 103  
 Db 593 SKSFDMITEHVRASLARMNTNNYDDK 619

RESULT 8  
 US-08-369-822C-25  
 Sequence 25, Application US/08369822C  
 Patent No. 6015660  
 GENERAL INFORMATION:  
 APPLICANT: Lipkin, W. I.  
 APPLICANT: Briese, Thomas  
 APPLICANT: Klische, Stefanie  
 APPLICANT: Schneider, Patrick A.  
 APPLICANT: Stitz, Lothar  
 APPLICANT: Schneemann, Anette  
 TITLE OF INVENTION: Borna Disease Viral Sequences, Diagnostics and Therapeutics for Central Nervous System Diseases  
 NUMBER OF SEQUENCES: 46  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Fulbright & Jaworski, L.L.P.  
 STREET: 865 South Figueroa Street, 29th Floor  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: USA  
 ZIP: 90017-2571  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: WINDOWS NT  
 SOFTWARE: ASCII (DOS) TEXT  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08369822C  
 FILING DATE: 06-JAN-1995  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Churchill, Margaret A. (Ph.D.)  
 REGISTRATION NUMBER: 39,944  
 REFERENCE/DOCKET NUMBER: 1279-194XX  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 213/992 9200  
 TELEFAX: 213/680-4518  
 INFORMATION FOR SEQ ID NO: 40:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 527 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear

RESULT 9  
 US-08-582-776C-40  
 Sequence 40, Application US/08582776C  
 Patent No. 607510  
 GENERAL INFORMATION:  
 APPLICANT: Lipkin, W. I.  
 APPLICANT: Briese, Thomas  
 APPLICANT: Klische, Stefanie  
 APPLICANT: Schneider, Patrick A.  
 APPLICANT: Stitz, Lothar  
 APPLICANT: Schneemann, Anette  
 TITLE OF INVENTION: Borna Disease Viral Sequences, Diagnostics and Therapeutics for Central Nervous System Diseases  
 NUMBER OF SEQUENCES: 61  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Fulbright & Jaworski, L.L.P.  
 STREET: 865 South Figueroa Street, 29th Floor  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: USA  
 ZIP: 90017-2576  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: WINDOWS NT  
 SOFTWARE: ASCII DOS TEXT  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/582.776C  
 FILING DATE: 04-JAN-1996  
 CLASSIFICATION: 435  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/434,831  
 FILING DATE: 04-MAY-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Churchill, Margaret A.  
 REGISTRATION NUMBER: 39,944  
 REFERENCE/DOCKET NUMBER: 1279-194C2  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 213/992 9200  
 TELEFAX: 213/680-4518  
 INFORMATION FOR SEQ ID NO: 40:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 527 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear

MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-582-776C-40

Query Match 11.2%; Score 70; DB 3; Length 527;  
Best Local Similarity 21.1%; Pred. No. 3.4; Mismatches 46; Indels 36; Gaps 5;  
Matches 27; Conservative 19; Mismatches 46; Indels 36; Gaps 5;

Best Local Similarity 21.1%; Pred. No. 3.4; Mismatches 46; Indels 36; Gaps 5;  
Matches 27; Conservative 19; Mismatches 46; Indels 36; Gaps 5;  
QY 7 FKKRSFAADRCKEVAQIRD---QHPSKIPVIER--YKGEKOLPVLDKTKFLVPHN 59  
Db 2,7 FESTALFGQRGCNEIFGKIFPPNMMHP---VLERCTIVGDPYCPVADRMHQLQJHAI 291

QY 60 MSELVKITIRRQLINPTQAFFLW-----NOHSMVSVSTIA 96  
Db 2,2 SGIFTHNPRGIE-GYCOQLWLTSMSAHLAAVAVGVGVRSAMVQGDNOIAIVTSRVPA 350

QY 47 DIVEQKD 104

Db 351 QTYKOKKN 358

RESULT 10

US-08-434-831B-37

Sequence 37, Application US/08434831B

Patent No. 6113905

GENERAL INFORMATION:

APPLICANT: Lipkin, W. I.

APPLICANT: Biiese, Thomas

APPLICANT: Kliche, Stefanie

APPLICANT: Schneider, Patrick A.

APPLICANT: Stitz, Lothar

APPLICANT: Schneemann, Annette

TITLE OF INVENTION: Borna Disease Viral Sequences, for Central Nervous

TITLE OF INVENTION: Diagnostics and Therapeutics for Central Nervous

TITLE OF INVENTION: System Diseases

NUMBER OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fulbright & Jaworski, L.L.P.

STREET: 865 South Figueroa Street, 29th Floor

CITY: Los Angeles

STATE: California

COUNTRY: USA

ZIP: 90017-2571

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: WINDOWS NT WORDPERFECT 8.0

SOFTWARE: ASCII (DOS) TEXT

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/434,831B

FILING DATE: 04-MAY-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/369,822

FILING DATE: 06-JAN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Churchill, Margaret A. (Ph.D.)

REFERENCE/DOCKET NUMBER: 1279-194C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 213/892-9200

TELEFAX: 213/680-4518

INFORMATION FOR SEQ ID NO: 37:

SEQUENCE CHARACTERISTICS:

LENGTH: 527 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

REGISTRATION NUMBER: 39,944

REFERENCE/DOCKET NUMBER: 1279-194C1

Query Match 11.2%; Score 70; DB 2; Length 589;

Best Local Similarity 22.6%; Pred. No. 3.9; Mismatches 50; Indels 20; Gaps 4;

Matches 28; Conservative 26; Mismatches 50; Indels 20; Gaps 4;

QY 6 PFKRSFAADRCKEVAQIRD---QHPSKIPVIER--YKGEKOLPVLDKTKFLVPHN 59

Db 73 PYKQRHNRQAEALIMQMLFLKVKMEI-----QGFLFLDQVQGLSYFQFLKQ 125

QY 66 IIR-----RRLQINPQIAFFLWQHSMVSVSP1ADYQEEKEDGFLYVMSV 116

Db 126 ILSSIHNEPRYFHNDLFLTAFKFLKQHG-NVSTWVDFKFLKQTSU-FNQANLW 181

QY 05-08-434-831B-37

Query Match 11.2%; Score 70; DB 3; Length 527;  
Best Local Similarity 21.1%; Pred. No. 3.4; Mismatches 46; Indels 36; Gaps 5;  
Matches 27; Conservative 19; Mismatches 46; Indels 36; Gaps 5;

QY 7 FESTALFGQRGCNEIFGKIFPPNMMHP---VLERCTIVGDPYCPVADRMHQLQJHAI 291

Db 60 MSELVKITIRRQLINPTQAFFLW-----NOHSMVSVSTIA 96

Db 292 SGIFTHNPRGIE-GYCOQLWLTSMSAHLAAVAVGVGVRSAMVQGDNOIAIVTSRVPA 350

QY 97 DIVEQKD 104

Db 351 QTYKOKKN 358

RESULT 11

US-08-937-540-6

Sequence 6, Application US/08437540

Patent No. 5891697

GENERAL INFORMATION:

APPLICANT: Croteau, Rodney B

APPLICANT: Wise, Mitchell L

APPLICANT: Savage, Thomas J

APPLICANT: Kattahira, Eya J

TITLE OF INVENTION: Monoterpene Synthases from Common Sage

TITLE OF INVENTION: (Salvia officinalis)

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: CHRISTENSEN, O'CONNOR, JOHNSON & KINDNESS

STREET: 1420 FIFTH AVENUE

CITY: SEATTLE

STATE: WASHINGTON

COUNTRY: USA

ZIP: 98101-2347

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/437,540

FILING DATE: 05-FEB-1995

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Sheldon, Dennis K

REGISTRATION NUMBER: 26,997

REFERENCE/DOCKET NUMBER: WSHR111254

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206 695 1718

TELEFAX: 206 224 0779

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 589 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US 08-937-540-6

Query Match 11.2%; Score 70; DB 2; Length 589;

Best Local Similarity 22.6%; Pred. No. 3.9; Mismatches 50; Indels 20; Gaps 4;

Matches 28; Conservative 26; Mismatches 50; Indels 20; Gaps 4;

QY 6 PFKRSFAADRCKEVAQIRD---QHPSKIPVIER--YKGEKOLPVLDKTKFLVPHN 59

Db 73 PYKQRHNRQAEALIMQMLFLKVKMEI-----QGFLFLDQVQGLSYFQFLKQ 125

QY 66 IIR-----RRLQINPQIAFFLWQHSMVSVSP1ADYQEEKEDGFLYVMSV 116

Db 126 ILSSIHNEPRYFHNDLFLTAFKFLKQHG-NVSTWVDFKFLKQTSU-FNQANLW 181

Db 182 DTKG 185

US-09-887-586A-54

RESULT 12  
 Sequence 54, Application US/09398395A  
 Patent No. 6468772  
 GENERAL INFORMATION:  
 APPLICANT: Chappell, Joseph  
 APPLICANT: No. 6468721, Joseph P.  
 APPLICANT: Starks, Courtney M.  
 APPLICANT: Manna, Kathleen R.  
 TITLE OF INVENTION: SYNTHASES  
 FILE REFERENCE: 07678-025001

CURRENT APPLICATION NUMBER: US/09/398, 395A  
 CURRENT FILING DATE: 1999-09-17  
 PRIOR APPLICATION NUMBER: 60/100, 993  
 PRIOR FILING DATE: 1998-09-18  
 PRIOR APPLICATION NUMBER: 60/130, 628  
 PRIOR FILING DATE: 1999-04-22  
 PRIOR APPLICATION NUMBER: 60/150, 262  
 PRIOR FILING DATE: 1999-08-23  
 NUMBER OF SEQ ID NOS: 58  
 SEQ ID NO 54  
 SOFTWARE: FastSEQ for Windows Version 3.0  
 LENGTH: 590

US-09-398-395A-54  
 Query Match 11.2%; Score 70; DB 4; Length 590;  
 Best Local Similarity 22.6%; Pred. No. 4;  
 Matches 28; Conservative 26; Mismatches 50; Indels 20; Gaps 4;

QY 6 PFKORRFAADRCKEVOQIRDQHPSKIPVIERVKGEKOLPVLDKTKFLVDPDHVNMSLVK 65  
 Db 73 PYKQRHNRQAEQIMQMLKVKMEAI-----QOLELIDDLQYIGLSFFQDEIKQ 125  
 QY 66 IIR-----RRLQLNPTQAFFLVNVQHSMVSVSTPIADTYEQEKEDEGFLYMYASQ 116  
 Db 126 ILSSIHNEPRYFHNDLFTALGFRILQHGF-NVSEDFDFCFKIEKCSD---FNAHLAQ 181

QY 117 ETFG 120  
 Db 182 DTKG 185

RESULT 14  
 Sequence 54, Application US/09895752  
 Patent No. 6559297  
 GENERAL INFORMATION:  
 APPLICANT: Chappell, Joseph  
 APPLICANT: No. 65592971, Joseph P.  
 APPLICANT: Starks, Courtney M.  
 APPLICANT: Manna, Kathleen R.  
 TITLE OF INVENTION: SYNTHASES  
 FILE REFERENCE: 07678-025001

CURRENT APPLICATION NUMBER: US/09/895, 752  
 CURRENT FILING DATE: 2001-06-29  
 PRIOR APPLICATION NUMBER: 09/398, 395  
 PRIOR FILING DATE: 1999-09-17  
 PRIOR APPLICATION NUMBER: 60/100, 993  
 PRIOR FILING DATE: 1998-09-18  
 PRIOR APPLICATION NUMBER: 60/130, 628  
 PRIOR FILING DATE: 1999-04-22  
 PRIOR APPLICATION NUMBER: 60/150, 262  
 PRIOR FILING DATE: 1999-08-23  
 NUMBER OF SEQ ID NOS: 58  
 SEQ ID NO 54  
 SOFTWARE: FastSEQ for Windows Version 3.0  
 LENGTH: 590

US-09-398-395A-54  
 Query Match 11.2%; Score 70; DB 4; Length 590;  
 Best Local Similarity 22.6%; Pred. No. 4;  
 Matches 28; Conservative 26; Mismatches 50; Indels 20; Gaps 4;

QY 6 PFKORRFAADRCKEVOQIRDQHPSKIPVIERVKGEKOLPVLDKTKFLVDPDHVNMSLVK 65  
 Db 73 PYKQRHNRQAEQIMQMLKVKMEAI-----QOLELIDDLQYIGLSFFQDEIKQ 125  
 QY 66 IIR-----RRLQLNPTQAFFLVNVQHSMVSVSTPIADTYEQEKEDEGFLYMYASQ 116  
 Db 126 ILSSIHNEPRYFHNDLFTALGFRILQHGF-NVSEDFDFCFKIEKCSD---FNAHLAQ 181

QY 117 ETFG 120  
 Db 182 DTKG 185

RESULT 13  
 Sequence 54, Application US/09887586A  
 Patent No. 6493534  
 GENERAL INFORMATION:  
 APPLICANT: Chappell, Joseph  
 APPLICANT: No. 6493541, Joseph P.  
 APPLICANT: Starks, Courtney M.  
 APPLICANT: Manna, Kathleen R.  
 TITLE OF INVENTION: SYNTHASES  
 FILE REFERENCE: 07678-025001

CURRENT APPLICATION NUMBER: US/09/887, 586A  
 CURRENT FILING DATE: 2001-06-22  
 PRIOR APPLICATION NUMBER: 09/398, 395  
 PRIOR FILING DATE: 1999-09-17  
 PRIOR APPLICATION NUMBER: 60/130, 628  
 PRIOR FILING DATE: 1999-04-22  
 PRIOR APPLICATION NUMBER: 60/150, 262  
 PRIOR FILING DATE: 1999-08-23  
 NUMBER OF SEQ ID NOS: 58  
 SEQ ID NO 54  
 SOFTWARE: FastSEQ for Windows Version 3.0  
 LENGTH: 590

US-09-887-586A-54  
 Query Match 11.2%; Score 70; DB 4; Length 590;  
 Best Local Similarity 22.6%; Pred. No. 4;  
 Matches 28; Conservative 26; Mismatches 50; Indels 20; Gaps 4;

QY 6 PFKORRFAADRCKEVOQIRDQHPSKIPVIERVKGEKOLPVLDKTKFLVDPDHVNMSLVK 65  
 Db 73 PYKQRHNRQAEQIMQMLKVKMEAI-----QOLELIDDLQYIGLSFFQDEIKQ 125  
 QY 66 IIR-----RRLQLNPTQAFFLVNVQHSMVSVSTPIADTYEQEKEDEGFLYMYASQ 116  
 Db 126 ILSSIHNEPRYFHNDLFTALGFRILQHGF-NVSEDFDFCFKIEKCSD---FNAHLAQ 181

QY 117 ETFG 120  
 Db 182 DTKG 185

RESULT 15  
 Sequence 54, Application US/09903012B  
 Patent No. 6569656  
 GENERAL INFORMATION:  
 APPLICANT: Chappell, Joseph  
 APPLICANT: No. 65696561, Joseph P.  
 APPLICANT: Starks, Courtney M.

US-09-903-012B-54  
 Query Match 11.2%; Score 70; DB 4; Length 590;  
 Best Local Similarity 22.6%; Pred. No. 4;  
 Matches 28; Conservative 26; Mismatches 50; Indels 20; Gaps 4;

QY 6 PFKORRFAADRCKEVOQIRDQHPSKIPVIERVKGEKOLPVLDKTKFLVDPDHVNMSLVK 65  
 Db 73 PYKQRHNRQAEQIMQMLKVKMEAI-----QOLELIDDLQYIGLSFFQDEIKQ 125  
 QY 66 IIR-----RRLQLNPTQAFFLVNVQHSMVSVSTPIADTYEQEKEDEGFLYMYASQ 116  
 Db 126 ILSSIHNEPRYFHNDLFTALGFRILQHGF-NVSEDFDFCFKIEKCSD---FNAHLAQ 181

QY 117 ETFG 120  
 Db 182 DTKG 185

US-09-903-012B-54  
 Query Match 11.2%; Score 70; DB 4; Length 590;  
 Best Local Similarity 22.6%; Pred. No. 4;  
 Matches 28; Conservative 26; Mismatches 50; Indels 20; Gaps 4;

QY 6 PFKORRFAADRCKEVOQIRDQHPSKIPVIERVKGEKOLPVLDKTKFLVDPDHVNMSLVK 65  
 Db 73 PYKQRHNRQAEQIMQMLKVKMEAI-----QOLELIDDLQYIGLSFFQDEIKQ 125  
 QY 66 IIR-----RRLQLNPTQAFFLVNVQHSMVSVSTPIADTYEQEKEDEGFLYMYASQ 116  
 Db 126 ILSSIHNEPRYFHNDLFTALGFRILQHGF-NVSEDFDFCFKIEKCSD---FNAHLAQ 181

QY 117 ETFG 120  
 Db 182 DTKG 185

US-09-903-012B-54  
 Query Match 11.2%; Score 70; DB 4; Length 590;  
 Best Local Similarity 22.6%; Pred. No. 4;  
 Matches 28; Conservative 26; Mismatches 50; Indels 20; Gaps 4;

QY 6 PFKORRFAADRCKEVOQIRDQHPSKIPVIERVKGEKOLPVLDKTKFLVDPDHVNMSLVK 65  
 Db 73 PYKQRHNRQAEQIMQMLKVKMEAI-----QOLELIDDLQYIGLSFFQDEIKQ 125  
 QY 66 IIR-----RRLQLNPTQAFFLVNVQHSMVSVSTPIADTYEQEKEDEGFLYMYASQ 116  
 Db 126 ILSSIHNEPRYFHNDLFTALGFRILQHGF-NVSEDFDFCFKIEKCSD---FNAHLAQ 181

QY 117 ETFG 120  
 Db 182 DTKG 185

US-09-903-012B-54  
 Query Match 11.2%; Score 70; DB 4; Length 590;  
 Best Local Similarity 22.6%; Pred. No. 4;  
 Matches 28; Conservative 26; Mismatches 50; Indels 20; Gaps 4;

QY 6 PFKORRFAADRCKEVOQIRDQHPSKIPVIERVKGEKOLPVLDKTKFLVDPDHVNMSLVK 65  
 Db 73 PYKQRHNRQAEQIMQMLKVKMEAI-----QOLELIDDLQYIGLSFFQDEIKQ 125  
 QY 66 IIR-----RRLQLNPTQAFFLVNVQHSMVSVSTPIADTYEQEKEDEGFLYMYASQ 116  
 Db 126 ILSSIHNEPRYFHNDLFTALGFRILQHGF-NVSEDFDFCFKIEKCSD---FNAHLAQ 181

QY 117 ETFG 120  
 Db 182 DTKG 185

; APPLICANT: Manna, Kathleen R.  
; TITLE OF INVENTION: SMITHASES  
; FILE REFERENCE: 07678-025001  
; CURRENT APPLICATION NUMBER: US/09/903, 012B  
; CURRENT FILING DATE: 2001-07-11  
; PRIOR APPLICATION NUMBER: 60/100, 993  
; PRIOR FILING DATE: 1999-09-18  
; PRIOR APPLICATION NUMBER: 60/130, 628  
; PRIOR FILING DATE: 1999-04-22  
; PRIOR APPLICATION NUMBER: 60/150, 262  
; PRIOR FILING DATE: 1999-08-23  
; NUMBER OF SEQ ID NOS: 58  
; SEQ ID NO 54  
; LENGTH: 590  
; TYPE: PRT  
; ORGANISM: Salvia officinalis  
; US-09-903-012B-54

Query Match Similarity 11.2%; Score 70; DB 4; Length 590;  
Best local similarity 22.6%; Pred. No. 4;  
Matches 28; Conservative 26; Mismatches 50; Indels 20; caps 4;  
Matches 28; Conservative 26; Mismatches 50; Indels 20; caps 4;  
Qy 6 PPKRSFADRKKEVQOIJRDQHPSKTRVIIERYKGKEKOLPVLUKTKLVLVDHVNMSSLVK 65  
Db 73 PPKRSFADRKKEVQOIJRDQHPSKTRVIIERYKGKEKOLPVLUKTKLVLVDHVNMSSLVK 65  
Qy 66 TIR-----RRLQINPNTAFLYVNOHSMVSVSPPIADYEQEKGDEGLYMYVASQ 116  
Db 126 TUSSTHNEPRYHNDIYFTALGFRLURQHGP-NVSEDFVDFKIECSD--FMANLAQ 181  
Qy 117 EFG 120  
Db 182 DFG 185

Search completed: August 11, 2003, 10:16:49  
Job time : 32 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 11, 2003, 10:15:34 ; Search time 53 Seconds

(without alignments)

290.617 Million cell updates/sec

Title: US-09-904-603-1

Perfect score: 625

Sequence: 1 MPSDRFFKQRSFADRCKEV..... EKDED3FLYNNVYASQETFGF 121

Scoring table: BL2SUM62

Gapext 10.0 , Gapext 0.5

Searched: 479057 seqs, 127295195 residues

Total number of hits satisfying chosen parameters: 479057

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%, Maximum Match 100%, Listing first 45 summaries

Database : Published\_Applications\_AA:\*

1: /cgn2\_6/ptodata/1/pubpaas/US07\_PUBCOMB.pep:\*

2: /cgn2\_6/ptodata/1/pubpaas/US08\_PUBCOMB.pep:\*

3: /cgn2\_6/ptodata/1/pubpaas/US09\_PUBCOMB.pep:\*

4: /cgn2\_6/ptodata/1/pubpaas/US09c\_PUBCOMB.pep:\*

5: /cgn2\_6/ptodata/1/pubpaas/US07\_NEW\_PUBCOMB.pep:\*

6: /cgn2\_6/ptodata/1/pubpaas/PCTUS\_PUBCOMB.pep:\*

7: /cgn2\_6/ptodata/1/pubpaas/US08\_NEW\_PUB.pep:\*

8: /cgn2\_6/ptodata/1/pubpaas/US08\_PUBCOMB.pep:\*

9: /cgn2\_6/ptodata/1/pubpaas/US09A\_PUBCOMB.pep:\*

10: /cgn2\_6/ptodata/1/pubpaas/US09B\_PUBCOMB.pep:\*

11: /cgn2\_6/ptodata/1/pubpaas/US09c\_PUBCOMB.pep:\*

12: /cgn2\_6/ptodata/1/pubpaas/US09\_NEW\_PUB.pep:\*

13: /cgn2\_6/ptodata/1/pubpaas/US10\_PUBCOMB.pep:\*

14: /cgn2\_6/ptodata/1/pubpaas/US10c\_PUBCOMB.pep:\*

15: /cgn2\_6/ptodata/1/pubpaas/US10c\_NEW\_PUB.pep:\*

16: /cgn2\_6/ptodata/1/pubpaas/US60\_NEW\_PUB.pep:\*

17: /cgn2\_6/ptodata/1/pubpaas/US60\_PUBCOMB.pep:\*

18: /cgn2\_6/ptodata/1/pubpaas/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score or the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

RESULT 1  
US-09-904-603-1  
; Sequence 1, Application US/0994603  
; Publication No. US20030099612A1  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; TITLE OF INVENTION: NOVEL MICROTUBULE ASSOCIATED PROTEIN  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/904,603  
; FILING DATE: 12-Jul-2001  
; CLASSIFICATION: <Unknown>  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: 088005,117  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Jerry J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0211 US  
TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-845-0155  
; TELEFAX: 415-845-4166  
; TELEX: <Unknown>  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:

LENGTH: 121 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

CLOSE: 144378

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

; US-09-904-603-1

Query Match Similarity 100.0%; Score 625; DB 11; Length 121;

Best Local Similarity 100.0%; Pred. No. 1. 2e-64; Mismatches 0; Indels 0; Gaps 0;

Matches 121; Conservative 0;

Qy 1 MPSDRPKQKRSFADRCKEVQOIQDRQHNSKIPVIERYKGEKOLPVLDKTFLVLPDHNM 60

Db 1 MPSDRPKQKRSFADRCKEVQOIQDRQHNSKIPVIERYKGEKOLPVLDKTFLVLPDHNM 60

Qy 61 SELVKIRRQLQNLPTQAFFLVLVNHMSWVSVSTPIADYEQEKEDGFLYMYVASQETFG 120

Db 61 SELVKIRRQLQNLPTQAFFLVLVNHMSWVSVSTPIADYEQEKEDGFLYMYVASQETFG 120

Qy 121 F 121

Db 121 F 121

RESULT 2

US-09-904-603-3

; Sequence 3, Application US/09904603

; GENERAL INFORMATION:

; APPLICANT: Hillman, Jennifer L.

; TITLE OF INVENTION: NOVEL MICROTUBULE-ASSOCIATED PROTEIN

; NUMBER OF SEQUENCES: 3

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FASTSEQ for Windows version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/904,603

; FILING DATE: 12-JUL-2001

; CLASSIFICATION: <unknown>

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: 08/605,117

; FILING DATE: <unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Billings, Lucy J.

; REFERENCE DOCKET NUMBER: 36,749

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-855-0555

; TELEFAX: 415-845-4166

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 142 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; IMMEDIATE SOURCE:

; LIBRARY: GenBank

; SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-09-904-603-3

Query Match Similarity 83.4%; Score 521; DB 11; Length 142;

Best Local Similarity 82.5%; Pred. No. 1. 5e-52; Mismatches 9; Indels 0; Gaps 0;

Matches 99; Conservative 12; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MPSDRPKQKRSFADRCKEVQOIQDRQHNSKIPVIERYKGEKOLPVLDKTFLVLPDHNM 60

Db 1 MPSDRPKQKRSFADRCKEVQOIQDRQHNSKIPVIERYKGEKOLPVLDKTFLVLPDHNM 60

Qy 61 SELVKIRRQLQNLPTQAFFLVLVNHMSWVSVSTPIADYEQEKEDGFLYMYVASQETFG 120

Db 61 SELVKIRRQLQNLPTQAFFLVLVNHMSWVSVSTPIADYEQEKEDGFLYMYVASQETFG 120

Qy 142 F 142

Db 142 F 142

RESULT 3

US-10-205-194-71

; Sequence 71, Application US/10205194

; GENERAL INFORMATION:

; APPLICANT: Warner-Lambert Company

; APPLICANT: Lee, Kevin

; APPLICANT: Dixon, Alistair

; APPLICANT: Brookbank, Robert

; APPLICANT: Pincock, Robert

; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain

; FILE REFERENCE: WIL-A-018201

; CURRENT APPLICATION NUMBER: US/10/205,194

; CURRENT FILING DATE: 5/20/07-24

; PRIORITY APPLICATION NUMBER: GB 0118354.0

; NUMBER OF SEQ ID NOS: 177

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO: 71

; LENGTH: 142

; TYPE: PRT

; ORGANISM: Rattus norvegicus

; FEATURE:

; OTHER INFORMATION: Light chain 3 subunit of microtubule-associated proteins 1A an

US-10-205-194-71

Query Match Similarity 83.4%; Score 521; DB 12; Length 142;

Best Local Similarity 82.5%; Pred. No. 1. 5e-52; Mismatches 9; Indels 0; Gaps 0;

Matches 99; Conservative 12; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MPSDRPKQKRSFADRCKEVQOIQDRQHNSKIPVIERYKGEKOLPVLDKTFLVLPDHNM 60

Db 1 MPSDRPKQKRSFADRCKEVQOIQDRQHNSKIPVIERYKGEKOLPVLDKTFLVLPDHNM 60

Qy 61 SELVKIRRQLQNLPTQAFFLVLVNHMSWVSVSTPIADYEQEKEDGFLYMYVASQETFG 120

Db 61 SELVKIRRQLQNLPTQAFFLVLVNHMSWVSVSTPIADYEQEKEDGFLYMYVASQETFG 120

Qy 142 F 142

Db 142 F 142

RESULT 4

US-09-925-301-1051

; Sequence 1051, Application US/09925301

; PATENT NO. US2002005308A1

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

; FILE REFERENCE: PA106

; CURRENT APPLICATION NUMBER: US/09/925,301

; CURRENT FILING DATE: 2001-08-10

; PRIORITY APPLICATION NUMBER: PCT/US00/05882

; PRIORITY FILING DATE: 2000-03-08

; PRIORITY APPLICATION NUMBER: 60/124,270

; NUMBER OF SEQ ID NOS: 1694

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO: 1051

; LENGTH: 171

; TYPE: PRT





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; PRIOR APPLICATION NUMBER: 60/253,625.
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SEQ ID NO: 12503
; LENGTH: 504
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-09-815-242-12503

Query Match 11:4%; Score 71; DB 9; length 504;
Best Local Similarity 19.8%; Pred. No. 9.6; Mismatches 26; Conservative 32; MisMatches 47; Indels 26; Gaps 6;
Matches 26

QY 8 KORRSFAADRCKEYQVQIRD-----QHPSKIFVILERYKEQKQI--PVLDKTKFLVVDH 57
Db 249 KNRKRMFETVKULETIDMEEFFDIDKQRPSEPTLDENNENNKKALAKSLRDLNTSNS 308
QY 58 VNKSELVKKIRR-RLQINPQAFPLVNOHMSVST-----P-TADIVESEKDEFG 108
Db 309 SUKTKVVKVKRDKIUSGKER--VKEPTKRSQPTVTEITKKPMSSIKQETKK-- 363
QY 109 LYMMVYASQETF 119
Db 364 - - IIYSSPQRF 372

RESULT 11
US-09-887-586A-54
; Sequence 54, Application US/09887586A
; Patent No. US20020094556A1

; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph P.
; APPLICANT: No. US20020094556A1, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/903,012
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 09/455,455
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,593
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/140,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 54
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Salvia officinalis
; US-09-903-012-54

Query Match 11:28; Score 70; DB 9; length 590;
Best Local Similarity 22.6%; Pred. No. 16; Mismatches 28; Conservative 26; MisMatches 50; Indels 20; Gaps 4;
Matches 28

QY 6 PFKQKSFADRKCKEYQVQIRD-----QHPSKIFVILERYKEQKQI--PVLDKTKFLVVDH 55
Db 73 PYKEQJRHENKQAEILMQRVMLKVKMEAI-----QOLELDDQYGLSYFFDEIKU 125
QY 66 IR-----RRIQLNFTQAFFLVLNQHMSVSTP-TADIVESEKDEFGLYMMVYASU 116
Db 126 ILSSIHNEPRYFHNNJLYTALGFHILKQHG-IVSHDVFCKEIKSUI--FNAJAU 181
QY 117 EFG 120
Db 182 DTKG 185

RESULT 13
US-09-900-799-54
; Sequence 54, Application US/099007997
; Publication No. US20030087406A1
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph P.
; APPLICANT: No. US20030087406A1, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/900,799
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: US/09/455,395
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 54
; LENGTH: 590
; TYPE: PRT
; ORGANISM: Salvia officinalis
; US-09-887-586A-54

Query Match 11:28; Score 70; DB 9; length 590;
Best Local Similarity 22.6%; Pred. No. 16; Mismatches 28; Conservative 26; MisMatches 50; Indels 20; Gaps 4;
Matches 28

QY 6 PFKQKSFADRKCKEYQVQIRD-----QHPSKIFVILERYKEQKQI--PVLDKTKFLVVDH 65
Db 73 PYKEQJRHENKQAEILMQRVMLKVKMEAI-----QOLELDDQYGLSYFFDEIKU 125
QY 66 IR-----RRIQLNFTQAFFLVLNQHMSVSTP-TADIVESEKDEFGLYMMVYASU 116
Db 126 ILSSIHNEPRYFHNNJLYTALGFHILKQHG-IVSHDVFCKEIKSUI--FNAJAU 181
QY 117 EFG 120
Db 182 DTKG 185

RESULT 13
US-09-900-799-54
; Sequence 54, Application US/099007997
; Publication No. US20030087406A1
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph P.
; APPLICANT: No. US20030087406A1, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/900,799
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: US/09/455,395
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 54
; LENGTH: 590
; TYPE: PRT
; ORGANISM: Salvia officinalis
; US-09-887-586A-54

```

US-09-900-797-54

Query Match Local Similarity 11.2%; Score 70; DB 11; Length 590;

Best Local Similarity 22.6%; Pred. No. 16; Mismatches 50; Indels 20; Gaps 4; Matches 28; Conservative 26; Mismatches 50; Indels 20; Gaps 4;

RESULT 15

US-10-177-293-375

; Sequence 375, Application US/10177293

; Publication No. US20030124128A1

; GENERAL INFORMATION:

; APPLICANT: Lillie, James

; APPLICANT: Glatt, Karen

; APPLICANT: Zhao, Xumei

; APPLICANT: Gannavarpu, Manjula

; APPLICANT: Kamattkar, Shubhangi

; APPLICANT: Mertens, Maureen

; APPLICANT: Myer, Vic

; APPLICANT: Wang, Youzhen

; APPLICANT: Xu, Yongrao

; APPLICANT: Hoersch, Sebastian

; APPLICANT: Monahan, John

; APPLICANT: Meyers, Rachel E.

; APPLICANT: Bast Jr., Robert C.

; APPLICANT: Horvagyi, Gabriel N.

; APPLICANT: Puszta, Lajos

; APPLICANT: Meric, Funda

; APPLICANT: Sahin, Aysegul

; APPLICANT: Mills, Gordon B.

; TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER

; FILE REFERENCE: MRI-038

; CURRENT APPLICATION NUMBER: US/10/177,293

; CURRENT FILING DATE: 2003-06-21

; PRIOR APPLICATION NUMBER: US 60/299,887

; PRIOR FILING DATE: 2001-06-21

; PRIOR APPLICATION NUMBER: US 60/301,572

; PRIOR FILING DATE: 2001-06-27

; PRIOR APPLICATION NUMBER: US 60/306,501

; PRIOR FILING DATE: 2001-07-18

; PRIOR APPLICATION NUMBER: US 60/325,002

; PRIOR FILING DATE: 2001-09-25

; PRIOR APPLICATION NUMBER: US 60/362,585

; PRIOR FILING DATE: 2002-03-05

; PRIOR APPLICATION NUMBER: US 60/xxx,xxx

; PRIOR FILING DATE: 2002-05-14

; NUMBER OF SEQ ID NOS: 506

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO: 375

; LENGTH: 362

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-10-177-293-375

; Query Match Local Similarity 11.0%; Score 68,5; DB 15; Length 362;

; Matches 24; Conservative 12; Mismatches 37; Indels 9; Gaps 3;

; Best Local Similarity 29.3%; Pred. No. 12; Mismatches 37; Indels 9; Gaps 3;

;保守性 19; Mismatches 39; Indels 89; Gaps 5;

Query Match Local Similarity 11.1%; Score 69,5; DB 10; Length 1233;

Best Local Similarity 18.8%; Pred. No. 48; Mismatches 34; Conservative 19; Mismatches 39; Indels 89; Gaps 5; Matches 34; Conservative 19; Mismatches 39; Indels 89; Gaps 5;

RESULT 14

US-09-626-4312

; Sequence 4312, Application US/09738626

; Publication No. US20020197605A1

; GENERAL INFORMATION:

; APPLICANT: Lillie, James

; APPLICANT: Glatt, Karen

; APPLICANT: Zhao, Xumei

; APPLICANT: Gannavarpu, Manjula

; APPLICANT: Kamattkar, Shubhangi

; APPLICANT: Mertens, Maureen

; APPLICANT: Meyers, Rachel E.

; APPLICANT: Bast Jr., Robert C.

; APPLICANT: Horvagyi, Gabriel N.

; APPLICANT: Puszta, Lajos

; APPLICANT: Xu, Yongrao

; APPLICANT: Hoersch, Sebastian

; APPLICANT: Monahan, John

; APPLICANT: Meyers, Rachel E.

; APPLICANT: Bast Jr., Robert C.

; APPLICANT: Horvagyi, Gabriel N.

; APPLICANT: Puszta, Lajos

; APPLICANT: Xu, Yongrao

; APPLICANT: Hoersch, Sebastian

; APPLICANT: Monahan, John

; APPLICANT: Meyers, Rachel E.

; APPLICANT: Bast Jr., Robert C.

; APPLICANT: Horvagyi, Gabriel N.

; APPLICANT: Puszta, Lajos

; APPLICANT: Xu, Yongrao

; APPLICANT: Hoersch, Sebastian

; APPLICANT: Monahan, John

; APPLICANT: Meyers, Rachel E.

; APPLICANT: Bast Jr., Robert C.

; APPLICANT: Horvagyi, Gabriel N.

; APPLICANT: Puszta, Lajos

; APPLICANT: Xu, Yongrao

; APPLICANT: Hoersch, Sebastian

; APPLICANT: Monahan, John

; APPLICANT: Meyers, Rachel E.

; APPLICANT: Bast Jr., Robert C.

; APPLICANT: Horvagyi, Gabriel N.

; APPLICANT: Puszta, Lajos

; APPLICANT: Xu, Yongrao

; APPLICANT: Hoersch, Sebastian

; APPLICANT: Monahan, John

; APPLICANT: Meyers, Rachel E.

; APPLICANT: Bast Jr., Robert C.

; APPLICANT: Horvagyi, Gabriel N.

; APPLICANT: Puszta, Lajos

; APPLICANT: Xu, Yongrao

; APPLICANT: Hoersch, Sebastian

; APPLICANT: Monahan, John

; APPLICANT: Meyers, Rachel E.

; APPLICANT: Bast Jr., Robert C.

; APPLICANT: Horvagyi, Gabriel N.

; APPLICANT: Puszta, Lajos

; APPLICANT: Xu, Yongrao

; APPLICANT: Hoersch, Sebastian

; APPLICANT: Monahan, John

; APPLICANT: Meyers, Rachel E.

Query Match Local Similarity 11.2%; Score 70; DB 11; Length 590;

Best Local Similarity 22.6%; Pred. No. 16; Mismatches 50; Indels 20; Gaps 4; Matches 28; Conservative 26; Mismatches 50; Indels 20; Gaps 4;

RESULT 15

US-10-177-293-375

; Sequence 375, Application US/10177293

; Publication No. US20030124128A1

; GENERAL INFORMATION:

; APPLICANT: Lillie, James

; APPLICANT: Glatt, Karen

; APPLICANT: Zhao, Xumei

; APPLICANT: Gannavarpu, Manjula

; APPLICANT: Kamattkar, Shubhangi

; APPLICANT: Mertens, Maureen

; APPLICANT: Meyers, Rachel E.

; APPLICANT: Bast Jr., Robert C.

; APPLICANT: Horvagyi, Gabriel N.

; APPLICANT: Puszta, Lajos

; APPLICANT: Xu, Yongrao

; APPLICANT: Hoersch, Sebastian

; APPLICANT: Monahan, John

; APPLICANT: Meyers, Rachel E.

; APPLICANT: Bast Jr., Robert C.

; APPLICANT: Horvagyi, Gabriel N.

; APPLICANT: Puszta, Lajos

; APPLICANT: Xu, Yongrao

; APPLICANT: Hoersch, Sebastian

; APPLICANT: Monahan, John

; APPLICANT: Meyers, Rachel E.

; APPLICANT: Bast Jr., Robert C.

; APPLICANT: Horvagyi, Gabriel N.

; APPLICANT: Puszta, Lajos

; APPLICANT: Xu, Yongrao

; APPLICANT: Hoersch, Sebastian

; APPLICANT: Monahan, John

; APPLICANT: Meyers, Rachel E.

; APPLICANT: Bast Jr., Robert C.

; APPLICANT: Horvagyi, Gabriel N.

; APPLICANT: Puszta, Lajos

; APPLICANT: Xu, Yongrao

; APPLICANT: Hoersch, Sebastian

; APPLICANT: Monahan, John

; APPLICANT: Meyers, Rachel E.

; APPLICANT: Bast Jr., Robert C.

; APPLICANT: Horvagyi, Gabriel N.

; APPLICANT: Puszta, Lajos

; APPLICANT: Xu, Yongrao

; APPLICANT: Hoersch, Sebastian

; APPLICANT: Monahan, John

; APPLICANT: Meyers, Rachel E.

; APPLICANT: Bast Jr., Robert C.

; APPLICANT: Horvagyi, Gabriel N.

; APPLICANT: Puszta, Lajos

; APPLICANT: Xu, Yongrao

; APPLICANT: Hoersch, Sebastian

; APPLICANT: Monahan, John

; APPLICANT: Meyers, Rachel E.

; APPLICANT: Bast Jr., Robert C.

; APPLICANT: Horvagyi, Gabriel N.

; APPLICANT: Puszta, Lajos

; APPLICANT: Xu, Yongrao

; APPLICANT: Hoersch, Sebastian

; APPLICANT: Monahan, John

; APPLICANT: Meyers, Rachel E.

Query Match Local Similarity 11.1%; Score 69,5; DB 10; Length 1233;

Best Local Similarity 18.8%; Pred. No. 48; Mismatches 34; Conservative 19; Mismatches 39; Indels 89; Gaps 5; Matches 34; Conservative 19; Mismatches 39; Indels 89; Gaps 5;

RESULT 14

US-09-626-4312

; Sequence 4312, Application US/09738626

; Publication No. US20020197605A1

; GENERAL INFORMATION:

; APPLICANT: Lillie, James

; APPLICANT: Glatt, Karen

; APPLICANT: Zhao, Xumei

; APPLICANT: Gannavarpu, Manjula

; APPLICANT: Kamattkar, Shubhangi

; APPLICANT: Mertens, Maureen

; APPLICANT: Meyers, Rachel E.

; APPLICANT: Bast Jr., Robert C.

; APPLICANT: Horvagyi, Gabriel N.

; APPLICANT: Puszta, Lajos

; APPLICANT: Xu, Yongrao

; APPLICANT: Hoersch, Sebastian

; APPLICANT: Monahan, John

; APPLICANT: Meyers, Rachel E.

; APPLICANT: Bast Jr., Robert C.

; APPLICANT: Horvagyi, Gabriel N.

; APPLICANT: Puszta, Lajos

; APPLICANT: Xu, Yongrao

; APPLICANT: Hoersch, Sebastian

; APPLICANT: Monahan, John

; APPLICANT: Meyers, Rachel E.

; APPLICANT: Bast Jr., Robert C.

; APPLICANT: Horvagyi, Gabriel N.

; APPLICANT: Puszta, Lajos

; APPLICANT: Xu, Yongrao

; APPLICANT: Hoersch, Sebastian

; APPLICANT: Monahan, John

; APPLICANT: Meyers, Rachel E.

; APPLICANT: Bast Jr., Robert C.

; APPLICANT: Horvagyi, Gabriel N.

; APPLICANT: Puszta, Lajos

; APPLICANT: Xu, Yongrao

; APPLICANT: Hoersch, Sebastian

; APPLICANT: Monahan, John

; APPLICANT: Meyers, Rachel E.

; APPLICANT: Bast Jr., Robert C.

; APPLICANT: Horvagyi, Gabriel N.

; APPLICANT: Puszta, Lajos

; APPLICANT: Xu, Yongrao

; APPLICANT: Hoersch, Sebastian

; APPLICANT: Monahan, John

; APPLICANT: Meyers, Rachel E.

; APPLICANT: Bast Jr., Robert C.

; APPLICANT: Horvagyi, Gabriel N.

; APPLICANT: Puszta, Lajos

; APPLICANT: Xu, Yongrao

; APPLICANT: Hoersch, Sebastian

; APPLICANT: Monahan, John

; APPLICANT: Meyers, Rachel E.

; APPLICANT: Bast Jr., Robert C.

; APPLICANT: Horvagyi, Gabriel N.

; APPLICANT: Puszta, Lajos

; APPLICANT: Xu, Yongrao

; APPLICANT: Hoersch, Sebastian

; APPLICANT: Monahan, John

; APPLICANT: Meyers, Rachel E.

ALIGNMENT

RESULT 3

Qy 1 MPSDRPEFKQRSFADRCRKEVQOIRDQHHSKIPVIIERYKGEEKOLPVLDKTKFLVDPDHNM 60  
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)  
 C;Accession: CB4887  
 C;Status: preliminary  
 R;Lin, X.; Kaul, S.; Rounseley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Talon, L.;  
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
 A;Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.  
 A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: B84470  
 A;Molecule type: DNA  
 A;Residues: 1-120 <STO>  
 A;Cross-references: GB:AE002093; NID:94581162; PIDN:AAD24645.1; GSPDB:GN00139  
 C;Genetics:  
 A;Gene: At2g0530  
 A;Map position: 2  
 C;Superfamily: hypothetical protein YBL078C

Query Match 36.3%; Score 227; DB 2; Length 120;  
 Best Local Similarity 37.7%; Pred. No. 3.5e-15;  
 Matches 43; Conservative 32; Mismatches 37; Indels 2; Gaps 2;

Qy 7 FKQRSSFADRCRKEVQOIRDQHHSKIPVIIERYKGEEKOLPVLDKTKFLVDPDHNMSELVKI 66  
 Db 6 FKHEHDLERKQAEAAIRAKTREKVPDRIPITVRAE-KSDVPHIDKRYLVPADTVQFQVIV 64

Qy 67 IRRRLQLNPTQAFFFLVNHQHMSVSVSTPIADYEQEKEDEGFLYMYASQETFG 120  
 Db 65 VRKKRKLSPERAKIFIFV-KNLLPPTAIMSAIEEKHDEGFLYMSYSGNTFG 117

RESULT 4

C84887 probable microtubule-associated protein [imported] - *Arabidopsis thaliana* (mouse-ear cress)  
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)  
 C;Accession: CB4887  
 C;Status: preliminary  
 R;Lin, X.; Kaul, S.; Rounseley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Talon, L.;  
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
 A;Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.  
 A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: CB4887  
 A;Molecule type: DNA  
 A;Residues: 1-122 <STO>  
 A;Cross-references: GB:AE002093; NID:94598366; PIDN:AAF18602.1; GSPDB:GN00139  
 C;Genetics:  
 A;Gene: At2g45170  
 A;Map position: 2  
 C;Superfamily: hypothetical protein YBL078C

Query Match 36.0%; Score 225; DB 2; Length 122;  
 Best Local Similarity 39.5%; Pred. No. 5.5e-15; Mismatches 47; Indels 12; Gaps 4;

Qy 19 EVQOIRDQHHSKIPVIIERYKGEEKOLPVLDKTKFLVDPDHNMSELVKIRRLQLNPTQ 78  
 Db 3 ESSRIRKVPDRIPIVKE-AQSDVPHIDKRYLVPADTVQFQVYVVRKRKLGAEKA 61

RESULT 5

Qy 61 SELVKIRRLQLNPTQAFFFLVNHQHMSVSVSTPIADYEQEKEDEGFLYMYASQETFG 120  
 Db 71 AEMLSIVRRRLQHPOQAFLFLVLYNERSMSVNSMSNLYSQERDPDGFWVMMVTSOPAFG 130

Query Match 35.0%; Score 219; DB 2; Length 107;  
 Best Local Similarity 39.2%; Pred. No. 1.8e-14; Mismatches 40; Indels 2; Gaps 2;

Qy 19 EVQOIRDQHHSKIPVIIERYKGEEKOLPVLDKTKFLVDPDHNMSELVKIRRLQLNPTQ 78  
 Db 3 ESSRIRKVPDRIPIVKE-AQSDVPHIDKRYLVPADTVQFQVYVVRKRKLGAEKA 61



Query Match 32.5%; Score 203; DB 2; Length 117;  
 Best Local Similarity 34.2%; Pred. No. 7.5e-13;  
 Matches 40; Conservative 30; Mismatches 39; Indels 8; Gaps 3;

QY 4 DRPFHQRRSFA DRCKEVQ QIRDQHRSKIPV IERYKG EKQLPVL DKTRFLV DHHVNNMSEL 63  
 Db 8 DHPEF YRK-----REGEKIRK KPYR P RVPV IVERK- RPKARV F D LDKKKYLV FSDLTVQF 60

QY 64 VKTIRRLQ NQPTQO FFLV NOHMSW VMSV STPIA D YBQEK D E GFLM VYAS QETFG 120  
 Db 61 YFLIKR KIHL R P E D A L F F F V N - N I P P T S A T M G Q L Y E D N H E E D Y F L V A Y S D E S V Y G 116

RESULT 11

T02148 hypothetical protein F8K4.23 - *Arabidopsis thaliana*  
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)  
 C;Accession: T02148 05-Mar-1999 #sequence\_revision 05-Mar-1999 #text\_change 22-Oct-1999  
 R;Vysotskai, V.S.; Schwartz, J.R.; Toriumi, M.; Kwan, A.; Yu, G.; Oji, O.; Liu, S.; Li, H.; Li, Y.; Palm, C.J.; Shinn, P.; Sun, H.; Davis, R.W.; Ecker, J.R.; Federspiel, N.; Ritz, D.; Miller, N.; submitted to the EMBL Data Library, August 1998  
 A;Description: *Arabidopsis thaliana* chromosome 1 BAC F8K4 sequence.  
 A;Reference number: Z14574  
 A;Accession: T02148  
 A;Status: translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-149 <VVS>  
 A;Cross-references: EMBL:AC004392; NID:g3282170; PID:93367536; PIDN: AAC28521.1; GSPDB:GN  
 C;Genetics: A;Gene: ATSP-F8K4.23  
 A;Introns: 13/1; 42/3; 60/2; 100/1; 128/1  
 C;Superfamily: hypothetical protein YBL078C

Query Match 32.2%; Score 201.5; DB 2; Length 149;  
 Best Local Similarity 33.6%; Pred. No. 1.4e-12;  
 Matches 42; Conservative 32; Mismatches 38; Indels 13; Gaps 3;

QY 7 F K Q R R S F A D R C K E V Q I R D Q H P S K I P ----- V I E R Y K G E K Q L P V I D K T K F L V P 55  
 Db 6 F K L E P L R Q E R R I S R R I S R E Y K P D R I P V M F S S I Y V I P C V I V E R R E - R S D V P N I D K K Y L V P 64

QY 56 D H V N S E L V I T R R Q L N T Q O F F I L V N D H M S V S V S T P I A D Y B Q E K D E G F L M V Y A S 115  
 Db 65 A D L T V G Q F V V V R K K I K L S R E K A I F V F V - K N T L P T A M M S A I Y D E N K D E D G F L M Y S G 123

QY 116 Q E T G G 120  
 Db 124 E N T F G 128

RESULT 12

T15740 hypothetical protein C32D5.9 - *Caenorhabditis elegans*  
 C;Species: *Caenorhabditis elegans*  
 C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 21-Jan-2000  
 C;Accession: T15740 R.Miller, N.  
 submitted to the EMBL Data Library, July 1995  
 A;Description: The sequence of *C. elegans* cosmid C32D5.  
 A;Reference number: Z18396  
 A;Accession: T15740  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-123 <MIL>  
 A;Cross-references: EMBL:U23511; NID:g746463; PID:g746472; PIDN: AAC46797.1; CESP: C32D5.9



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**KW** Microtubules. 0 0 MW. BY SIMILARITY.  
**FT** INIT-MET 141 AA; 16263 MW; F14E9D708D03D65D CRC64;  
**SEQUENCE** 141 AA; 16263 MW; F14E9D708D03D65D CRC64;  
**Query Match** Score 82.6%; Score 516; DB 1; Length 141;  
**Best Local Similarity** 82.4%; Pred. No. 4e-45;  
**Matches** 98; Conservative 12; Mismatches 9; Indels 0; Gaps 0;  
**QY** 2 PSDRDPKQRTSFADRCRKEVQDHPSKPVITERYKGKQLPVLDTKTFKLVPDHVMS 61  
**Db** 1 PSEKTPKQRTSFADRCRKEVQDHPSKPVITERYKGKQLPVLDTKTFKLVPDHVMS 60  
**QY** 62 ELVKIRRQLNPQAFFFLVQHNSMVSSTPADIYEDEKDEGFLINVAQSTFG 120  
**Db** 61 ELIKIRRQLNQAFFFLVQHNSMVSSTPISEVYESERDEGFLVQVYASQETFG 119

**RESULT 6**  
**YHM5\_CAEEL** STANDARD; PRT: 130 AA.  
**ID** YHM5\_CAEEL  
**AC** Q23536;  
**DT** 15-JUL-1998 (Rel. 36, created)  
**DT** 15-JUL-1998 (Rel. 36, Last sequence update)  
**DT** 16-OCT-2001 (Rel. 40, Last annotation update)  
**DE** Hypothetical 15.1 kDa protein ZK593.6 in chromosome IV.  
**GN** ZK593.6  
**OS** Caenorhabditis elegans.  
**OC** Bokaryota; Metazoa; Chromadorea; Rhabditida; Rhabditoidea;  
**OC** Rhabditidae; Pseudorinae; Caenorhabditis.  
**OX** NCBI\_TAXID=6239;  
**RN** [1]  
**RP** SEQUENCE FROM N.A.  
**RC** STRAIN-Bristol N2;  
**RA** McMurray A.;  
**RL** Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.  
**CC** -!- SIMILARITY: BELONGS TO THE MAP1 LC3 / GEF2 FAMILY.  
**CC** This SWISS-PROT entry is copyright. It is produced through a collaboration  
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**CC** entities requires a license agreement. (See <http://www.isb-sib.ch/announce/>  
**CC** or send an email to license@isb-sib.ch).  
**DR** InterPro: IPR00421.1; -;  
**DR** WormPep: ZK593.6; CE06627;  
**DR** InterPro: IPR00421.1;  
**DR** Pfam: PF02991; MAP1LC3;  
**DR** Hypothetical protein;  
**KW** SEQUENCE 130 AA; 15095 MW; 347518D8C8D3154 CRC64;

**Query Match** Score 61.0%; Score 381.5; DB 1; Length 130;  
**Best Local Similarity** 56.3%; Pred. No. 1.3e-31;  
**Matches** 70; Conservative 27; Mismatches 20; Indels 3; Gaps 1;

**QY** 1 MPSDRPKQRTSFADRCRKEVQDHPSKPVITERYKGKQLPVLDTKTFKLVPDHVMS 60  
**Db** 14 VPS--FKRPFHFRQKVEEIRSQQPKVNPVIERFERSPLMPLRCKFLYEHITV 70

**QY** 61 SELVKIRRQLNPQAFFFLVQHNSMVSSTPADIYEDEKDEGFLINVAQSTFG 120  
**Db** 71 AELMSIVRRLQHLQQAFPLLVNERSMSMSMSNLYSQERPDGDFVMMVTSQARG 130

**RESULT 7**  
**GEF2\_HUMAN** STANDARD; PRT: 117 AA.  
**ID** 009765; 09DCB8; Q9UQF7;  
**AC** 15-JUL-1998 (Rel. 36, Created)  
**DT** 15-JUL-1998 (Rel. 36, Last sequence update)  
**DT** 15-SEP-2003 (Rel. 42, Last annotation update)

**DE** Ganglioside expression factor 2 (GEF-2) (General protein transport factor p16) (GABA(A) receptor-associated protein-like 2)  
**DE** (MAP1 light chain 3 related protein).  
**DE** GABARpL2 or GEF2 or FLC3A.  
**GN**  
**OS** Homo sapiens (Human);  
**OS** Mus musculus (Mouse);  
**OS** Rattus norvegicus (Rat), and  
**OS** Bos taurus (Bovine).  
**OS** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
**OS** Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.  
**OX** NCBI\_TAXID=9606, 10090, 10116, 9913;  
**RN** [1]  
**RP** SEQUENCE FROM N.A.  
**RC** SPECIES=Human;  
**RC** Storch S., Brulke T.;  
**RL** Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.  
**RN** [2]  
**RP** SEQUENCE FROM N.A.  
**RC** SPECIES=Human; TISSUE=Pituitary;  
**RA** Song H., Peng Y., Yu Y., Fu G., Mao M., Zhang Q., Zhu H., Li G.,  
**RA** Luo M., Chen J., Hu R.;  
**RT** "Human GEF2 homolog gene";  
**RL** Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
**RN** [3]  
**RP** SEQUENCE FROM N.A., AND INTERACTION WITH ULK1.  
**RC** SPECIES=Human; TISSUE=Frontal cortex;  
**RX** MEDLINE=201065693; PubMed=11146101;  
**RA** Okasaki N., Yan J., Yuspa S., Ueno T., Kominami E., Masuho Y.,  
**RA** Koga H., Muramatsu M. A.;  
**RT** "Interaction of the Unc-51-like kinase and microtubule-associated  
**RT** protein light chain 3 related proteins in the brain: possible role of  
**RT** vesicular transport in axonal elongation.;"  
**RL** Brain Res. Mol. Brain Res. 85:1-12(2000).  
**RN** [4]  
**RP** SEQUENCE FROM N.A.  
**RC** SPECIES=Human; TISSUE=Brain, and Testis;  
**RA** Strausberg R.;  
**RL** Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
**RN** [5]  
**RP** SEQUENCE FROM N.A.  
**RC** SPECIES=Human, and Mouse;  
**RX** MEDLINE=2139076; PubMed=111414770;  
**RA** Xin Y., Yu L., Chen Z., Zheng L., Fu Q., Jiang J., Zhang P., Gong R.,  
**RA** Zhao S.;  
**RT** "Cloning, expression patterns, and chromosome localization of three  
**RT** human and two mouse homologues of GABA(A) receptor-associated  
**RT** protein.;"  
**RL** Genomics 74:408-413(2001).  
**RN** [6]  
**RP** SEQUENCE FROM N.A.  
**RC** SPECIES=Rat; TISSUE=Brain;  
**RA** Ogura K.;  
**RL** Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.  
**RN** [7]  
**RP** SEQUENCE FROM N.A.  
**RC** SPECIES=Bovine; TISSUE=Brain;  
**RX** MEDLINE=20211392; PubMed=10747018;  
**RA** Sagiv Y., Leiberman-Miller A., Porat A., Elazar Z.;  
**RT** "Gapt-16, a membrane transport modulator, interacts with NSF and the  
**RT** Golgi v-SNARE GOS-28.;"  
**RL** EMBO J. 19:1494-1504(2000).  
**RN** [8]  
**RP** SEQUENCE FROM N.A.  
**RC** SPECIES=Bovine; TISSUE=Kidney;  
**RX** MEDLINE=2230861; PubMed=12438634;  
**RA** Becher P., Thiel H.-J., Collins M., Brownlie J., Orlich M.;  
**RT** "Cellular sequences in pestivirus genomes encoding gamma-aminobutyric  
**RT** acid (A) receptor-associated protein and Golgi-associated ATPase  
**RT** enhancer of 16 kilodaltons.;"  
**J. Virol.** 76:13069-13076(2002).  
**RN** [9]  
**RP** SEQUENCE FROM N.A.  
**RC** SPECIES=Mouse; STRAIN=C57BL/6J; TISSUE=Hippocampus, and Kidney;



Db 5 FKDEHPFEKKRKAERIROYKDPRIPIVCK-ADRTDIPITDKKKYLVPSDLTVQGOFVIV 63  
 Qy 67 IRRQLQNLNTQAFELLVNHSMWSVSTPLADTYEQEKGDFLIMVYASQETFG 120  
 Db 64 IRKRIKLAPEKAIFLFDVE-VLPPTAALMSAIEHKDDENFLYVSYSGENTFG 116  
 RESULT 9  
 APG8\_YEAST STANDARD; PRT; 117 AA.  
 ID APG8\_YEAST AC P31182; DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DE Autophagy protein 8 (Contains: Apq8FG).  
 APG8 OR AUT7 OR YBL078C OR YBL0732.  
 OS Saccharomyces cerevisiae (Baker's Yeast).  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
 OC Eukaryota; Fungi; Ascomycota; Saccharomyces.  
 OC Saccharomyces cerevisiae (Baker's Yeast).  
 OC NCBI\_TaxID=4932; [1]  
 SEQUENCE FROM N.A.  
 STRAIN=S288C; RC STRAIN=S288C; RX STRAIN=96076635; PubMed=7502586;  
 RA Obermaier B., Gassnerhuber J., Piravandi R., Domdey H.;  
 RT "Sequence analysis of a 7.86 kb segment of the left end of Saccharomyces cerevisiae chromosome III.";  
 RL Yeast 11:1103-1112(1995).  
 [2]  
 SEQUENCE FROM N.A.  
 STRAIN=S288C; RC STRAIN=S288C; RX STRAIN=S288C; RA Contreras R., Fiers W., Logghe M., Moelmans F.;  
 RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP CHARACTERIZATION.  
 MEDLINE=2049280; PubMed=11038174;  
 RA Kirisako T., Ichimura Y., Okada H., Kubota Y., Mizushima N., Yoshimori T., Onsumi M., Takao T., Noda T., Ohsumi Y.;  
 RT "The reversible modification regulates the membrane-binding state of Apq8/Aut7 essential for autophagy and the cytoplasm to vacuole targeting pathway";  
 RL J. Cell Biol. 151:263-276(2000).  
 CC --!- FUNCTION: Forms a protein complex with AUT2 to mediate attachment of autophagosomes to microtubules.  
 CC --!- SUBCELLULAR LOCATION: Membrane-bound.  
 CC --!- PTM: The C-terminal Arg of Apq8 is removed by Apq4 to form Apq8FG. Apq8FG forms a conjugate with an unidentified molecule "X" and thereby binds tightly to membranes. The adduct Apq8FG-X is reversed to soluble or loosely membrane-bound Apq8FG by cleavage by Apq4.  
 CC --!- SIMILARITY: BELONGS TO THE MAP1 LC3 / GEF2 FAMILY.  
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 CC DR 023511; AAC6797\_1; --!  
 CC DR EMBL; AF326943; XAG49393\_1; -.  
 CC DR PIR; T15740; T15740.  
 CC DR WormPep; C3205\_9; CE01849.  
 CC DR InterPro; IPR004241; MAP1\_LC3.  
 CC DR Pfam; PF02991; MAP1\_LC3; 1.  
 CC KW Hypothetical protein.  
 SQ SEQUENCE 123 AA; 14764 MW; BC08172A3101875A CRC64;  
 CC  
 DR EMLU; X79489; CAAS6032\_1; -.  
 DR EMLU; Z35839; CAAB4899\_1; -.  
 DR PIR; S45422; S4532.  
 DR SGD; S000014; AUT7.  
 DR GO; GO:0005875; C:microtubule associated complex; IPI.  
 DR GO; GO:0008017; F:microtubule binding activity; IPI.  
 DR GO; GO:006914; P:autophagy; IGL.  
 DR GO; GO:006633; P:protein-vacuolar targeting; IMP.  
 DR Pfam; PF02991; MAP1\_LC3; 1.  
 KW Autophagy; Membrane; Ubi conjugation pathway.  
 DOMAIN 1  
 FT SITE 116 117 CLIVAGE (BY APG4).  
 FT SEQUENCE 117 AA; 13627 MW; 1246CEFF5AU38819 CRC64;  
 SQ  
 RESULT 10  
 YOD9\_CAEEL STANDARD; PRT; 123 AA.  
 ID YOD9\_CAEEL AC Q05490; DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DE Hypothetical protein C32D5.9 in chromosome II.  
 OS Cenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peidorinida; Caenorhabditis.  
 OC NCBI\_TaxID=6239; [1]  
 SEQUENCE FROM N.A.  
 STRAIN=Bristol N2; RC STRAIN=Bristol N2; RA Miller N;  
 RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 STRAIN=Bristol N2; RC STRAIN=Bristol N2; RA Kollar A.Y., Shin-i.T., Suzuki Y., Sugano S., Potdevin M., Thierry-Mieg Y., Thierry-Mieg D., Thierry-Mieg J.;  
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
 CC --!- SIMILARITY: BELONGS TO THE MAP1 LC3 / GEF2 FAMILY.  
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 CC DR EMBL; AF326943; XAG49393\_1; -.  
 CC DR PIR; T15740; T15740.  
 CC DR WormPep; C3205\_9; CE01849.  
 CC DR InterPro; IPR004241; MAP1\_LC3.  
 CC DR Pfam; PF02991; MAP1\_LC3; 1.  
 CC KW Hypothetical protein.  
 SQ SEQUENCE 123 AA; 14764 MW; BC08172A3101875A CRC64;  
 CC  
 DR EMLU; X79489; CAAS6032\_1; -.  
 DR EMLU; Z35839; CAAB4899\_1; -.  
 DR PIR; S45422; S4532.  
 DR SGD; S000014; AUT7.  
 DR GO; GO:0005875; C:microtubule associated complex; IPI.  
 DR GO; GO:0008017; F:microtubule binding activity; IPI.  
 DR GO; GO:006914; P:autophagy; IGL.  
 DR GO; GO:006633; P:protein-vacuolar targeting; IMP.  
 DR Pfam; PF02991; MAP1\_LC3; 1.  
 KW Autophagy; Membrane; Ubi conjugation pathway.  
 DOMAIN 1  
 FT SITE 116 117 CLIVAGE (BY APG4).  
 FT SEQUENCE 117 AA; 13627 MW; 1246CEFF5AU38819 CRC64;  
 SQ  
 RESULT 11  
 DNLL\_CHLMU STANDARD; PRT; 660 AA.  
 ID DNLL\_CHLMU

AC Q9PKP4;  
 DT 16-OCT-2001 (Rel. 40, created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DE DNA ligase (EC 6.5.1.2) (Polydeoxyribonucleotide synthase (NAD<sup>+</sup>)).  
 GN LIGA (PR ID:423.  
 OS *Chlamydia muridarum*.  
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.  
 OX NCBI\_TAXID=83560;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MOPN / Nigg;  
 RX MEDLINE=20150255; PubMed=10684935;  
 RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,  
 White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,  
 RA Linher K., Weidman J., Khouri H., Craven R., Bowman C., Dodson R.,  
 Gwin M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,  
 RA Eisen J., Fraser C.M.,  
 RT *\*Genome sequences of Chlamydia trachomatis Mopn and Chlamydia*  
 RT *pneumoniae Ar39.*;  
 RL *Nucleic Acids Res.* 28:1397-1406(2000).  
 CC *-!- FUNCTION: THIS PROTEIN CATALYZES THE FORMATION OF PHOSPHODESTER*  
 CC *LINKAGES BETWEEN 5'-PHOSPHORYL AND 3'-HYDROXYL GROUPS IN DOUBLE-*  
 CC *STRANDED DNA USING NAD AS A COENZYME AND AS THE ENERGY SOURCE FOR*  
 CC *THE REACTION. IT IS ESSENTIAL FOR DNA REPLICATION AND REPAIR OF*  
 CC *DAMAGED DNA. (BY SIMILARITY).*  
 CC *-!- CATALYTIC ACTIVITY: NAD(+)* + {deoxyribonucleotide}(N) \* {deoxyribonucleotide}(N) \* {deoxyribonucleotide}(N<sup>+</sup>M) = AMP + nicotinamide nucleotide .  
 CC *-!- SIMILARITY: BELONGS TO THE NAD-DEPENDENT DNA LIGASE FAMILY.*  
 CC *-!- SIMILARITY: Contains 1 BRCT domain.*  
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 EMBL: AE002309; AAC39279.1;  
 DR PIR: A81704; A81704.  
 DR HSSP: 08703; IB04.  
 DR InterPro: IPR00423; .  
 DR InterPro: IPR001357; BRCT.  
 DR InterPro: IPR004150; DNA\_ligase\_OB.  
 DR InterPro: IPR001679; DNA\_ligase.  
 DR InterPro: IPR00045; HhH  
 DR InterPro: IPR003583; HhH\_1.  
 DR InterPro: IPR004149; Znt\_DNA\_ligase\_C4.  
 DR Pfam: PF00533; BRCT\_1.  
 DR Pfam: PF01653; DNA\_ligase\_N; 1.  
 DR Pfam: PF03120; DNA\_ligase\_QB; 1.  
 DR Pfam: PF03119; DNA\_Ligase\_ZBD; 1.  
 DR Pfam: PF00633; HhH; 1.  
 DR Prodom: P000344; DNALigase; 1.  
 DR SMART: SM00292; BRCT; 1.  
 DR SMART: SM00278; HhH; 1.  
 DR SMART: SM00532; LIG4NC; 1.  
 DR TIGRFAMs: TIGR00575; dn1; 1.  
 DR PROSITE: PS50172; BRCT; 1.  
 DR PROSITE: PS01055; DNA\_LIGASE\_N1; FALSE\_NEG.  
 DR PROSITE: PS01056; DNA\_LIGASE\_N2; 1.  
 KW Ligase; DNA repair; DNA replication; NAD; Complete proteome.  
 FT DOMAIN 581 660 AMP (BY SIMILARITY);  
 FT BINDING 114 114 AMP (BY SIMILARITY);  
 SQ SEQUENCE 660 AA; 73784 MW; 06EBB9155E723EAD C0564;  
 SP 11 9%; Score 74.5; DB 1; Length 560;  
 Best Local Similarity 24.5%; Pred. No. 7.5;  
 Matches 26; Conservative 16; Mismatches 27; Index 37; Gaps 3;  
 CC *-!- TISSUE SPECIFICITY: IN STEM, CAULINE LEAVES, ROOTS AND FLOWERS.*  
 CC *-!- LOW LEVELS FOUND IN MATURING SEEDS. ABSENT IN FRY SEEDS.*

RESULT 12

DR DH10\_ARATH

ID DH10\_ARATH

STANDARD; PRI; 260 AA.

AC P42759;

DT 01-NOV-1995 (Rel. 32, created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DE Dehydrin\_ERD10 (Low-temperature-induced protein LT145).

GN ERD10 OR LT145 OR LT129 OR AT1G20050 OR F5M15.21.

OS *Arabidopsis thaliana* (Mouse-ear cress).

OC *Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Rosidae: eurosid I: Brassicales: Brassicaceae: Arabidopsis.*

OX NCBI\_TAXID=3702;

RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN=cv\_ Columbia;

RX MEDLINE=9434873; PubMed=80649191;

RA Kyuoco T., Yamauchi-Shinozaki K., Shinozaki K.;

RC "Characterization of two cDNAs (ERD10 and ERD14) corresponding to genes that respond rapidly to dehydration stress in *Arabidopsis thaliana*." Plant Cell Physiol. 35:225-231(1994).

RN [2]  
 RP SEQUENCE FROM N.A.

RC STRAIN=cv\_ *Landsberg erecta*; TISSUE: leaf;

RX MEDLINE=96046757; PubMed=7579189;

RA Wellin B.V., Olson A., Palva E.T.; "Structure and organization of two closely related low-temperature-induced dn1/leaf/1a-like genes in *Arabidopsis thaliana* L. *Heynh.*"; Plant Mol. Biol. 29:391-395(1995).

RN [3]  
 RP SEQUENCE FROM N.A.

RC STRAIN=cv\_ Columbia;

RX MEDLINE=21016719; PubMed=11130712;

RA Theologis A., Becker J.R., Palm C.J., Fedderspiel N.A., Kaul S., White O., Alonso J., Altschuler R., Araujo R., Bowman C.L., Brooks S.Y., Buehler E., Chan A., Chao U., Chen H., Cheuk R.F., Chin C.W., Chung M.K., Conn L., Conway A.R., Creasy T.H., Hewitt R., Dunn P., Eguu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii T.Y., Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huijzer L., Hunter J.L., Johnson-Hopson C., Khan S., Khaykin E., Kim C.J., Koo H.L., Krennenstuhl L., Kurtz D.B., Kwan A., Lam B., Langin-Hooper S., Lee A., Lee J.-M., Leu C.A., Li J.-H., Li Y.-P., Lin X., Lin S.-X., Liu Z.-A., Luro J.-S., Maiti R., Marzali A., Millischer J., Miranda M., Nazyren M., Nierman W.C., Osborne B.I., Pai G., Peterson J., Phan P.K., Rizzo M., Rooney T., Rowley Jr., Sakano H., Salberg S., Schwartz J.R., Shin P., Southwick A.M., Sun H., Taliou L.J., Tamouda G., Toriumi M.J., Town C.D., Utterback T., Van Arken S., Vanberg M., Vysotskaya V.S., Walker M., Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W., RT "Sequence and analysis of chromosome 1 of the plant *Arabidopsis thaliana*." RT *Nature* 408:816-820(2000).

RN [4]  
 RP SEQUENCE OF 56-260 FROM N.A.

RC STRAIN=cv\_ *Landsberg erecta*; ISSUE: 1;cat;

RX MEDLINE=95035955; PubMed=7948863;

RA Wellin B.V., Olson A., Nylander M., Palva E.T.; "Characterization and differential expression of dn1/leaf/1a/1b-like genes during cold acclimation and drought stress in *Arabidopsis thaliana*." Plant Mol. Biol. 26:131-144(1994).





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GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: August 11, 2003, 10:08:18 ; Search time 95 Seconds

Scoring table: BLOSUM62 ; Gapext 0.0 ; Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0.8 ; Maximum Match 100% ; Listing first 45 summaries

Database : SPREMBL\_23 ; \*

1: sp\_archaea;\*  
2: sp\_bacteria;\*  
3: sp\_fungi;\*  
4: sp\_human;\*  
5: sp\_invertebrate;\*  
6: sp\_mammal;\*  
7: sp\_mhc;\*  
8: sp\_organelle;\*  
9: sp\_phage;\*  
10: sp\_plant;\*  
11: sp\_rabbit;\*  
12: sp\_virus;\*  
13: sp\_vertebrate;\*  
14: sp\_unclassified;\*  
15: sp\_rvirus;\*  
16: sp\_bacteriap;\*  
17: sp\_archeap;\*

Pred No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	625	106.0	121	4	Q9BXW5
2	625	100.0	121	11	Q91VR7
3	625	100.0	170	4	Q9H491
4	622	99.5	121	11	Q9DC74
5	359	57.4	147	4	Q9BXW4
6	242	38.7	339	12	Q8B512
7	234	37.4	116	10	Q8H715
8	234	37.4	121	10	Q8VK7
9	230	36.8	120	10	Q8LB9
10	227	36.3	120	10	Q9SL04
11	222	36.3	122	10	Q945K6
12	227	36.3	122	10	Q8LEM4
13	226	36.2	122	10	Q8S928
14	225	36.2	122	10	Q8S226
15	224	35.8	121	3	Q94272
16	223	35.7	115	10	Q9LRP7

RESULT 1

Q9BXW5

ID Q9BXW5; PRELIMINARY; PRT; 121 AA.

AC Q9BXW5; DT 01-JUN-2001 (REMBL; 17, Last sequence update); DT 01-JUN-2001 (REMBL; 17, Last annotation update); DT 01-OCT-2002 (REMBL; 22, Last annotation update); DE MAP1 light chain 3-like protein 1 (Hypothetical protein). GN DKFZP761L0515.

OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; NCBI-TaxID=9606;

RN [1] RA SEQUENCE FROM N. A.  
RA Yu L.;  
RN [2] RA Submitted (JUN 2000) to the EMBL/GenBank/DBJ databases.  
RN [2] RA SEQUENCE FROM N. A.

RC TISSUE=uterus; RA Strasbourg R.;  
RL Submitted (JUL 2001) to the EMBL/GenBank/DBJ databases.  
RN [3] RA SEQUENCE FROM N. A.  
RC TISSUE=Amygda; RA Ansorge W., Winkner U., Mewes H. W., Weil B., Wiemann S.; RL Submitted (JUL 2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF216658; AACR5151; -;  
DR EMBL: BC015810; AAH15810; 1; -;  
DR EMBL: AL833855; CAD3871; 1; -;  
DR InterPro: IPR004241; MAP1\_LC3;  
DR Pfam: PF02991; MAP1\_LC3; 1;  
KW HYPOTHETICAL PROTEIN;  
SQ SEQUENCE: 121 AA: 14272 MW: 481188478942E3 CR:64;

Query Match 100.0%; Score 625; UB 4; Length 121;  
Best Local Similarity 100.0%; Pred. No. 1.5e-55;  
Matches 121; Conservative 0; Mismatches 0; Index S 0.0; CDS 0.0; MinS 0.0;

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Db	1 MPSDRPKQRRSFADRCKEVQIQRDQHPSKIPVILERYKEKQLVPLDKTKFLVPHVM 60	SEQUENCE	170 AA;	19189 MW;	BBCT7521FDC6E4823	CRC64;
QY	61 SELVKIRRQLQNLNTQAFLLVNVQHSMWSVSTPIADIYEQEKGFLYMWVQSETRG 120	Query Match	100.0%	Score 625;	DB 4;	Length 170;
Db	61 SELVKIRRQLQNLNTQAFLLVNVQHSMWSVSTPIADIYEQEKGFLYMWVQSETRG 120	Best Local Similarity	100.0%	Pred. No. 2.3e-56;	0;	
Db	121 F 121	Matches 121;	Conservative	0;	Mismatches 0;	Indels 0;
RESULT 2		Deletions 0;	Gaps 0;	Score 0;	DB 0;	
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AC Q91VR7;						
DT 01-DEC-2001 (TREMBlrel. 19, Created)						
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)						
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)						
DE MAP1 light chain 3-like protein 1.						
OS Mus musculus (Mouse)						
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
RA Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.						
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SEQUENCE FROM N.A.						
TISSUE=Breast tumor;						
Strausberg R.;						
Submitter (JUL-2001) to the EMBL/GenBank/DBJ databases.						
DR EMBL; BCO10596; AAH10596.1; -.						
DR InterPro; IPR04441; MAP1_LC3.						
DR InterPro; IPR02991; MAP1_LC3.						
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DR InterPro; IPR02991; MAP1_LC3.						
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Db	1 MPSDRPKQRRSFADRCKEVQIQRDQHPSKIPVILERYKEKQLVPLDKTKFLVPHVM 60	ID Q9DC74				
QY	1 MPSDRPKQRRSFADRCKEVQIQRDQHPSKIPVILERYKEKQLVPLDKTKFLVPHVM 60	AC Q9PC74;				
Db	50 MPSDRPKQRRSFADRCKEVQIQRDQHPSKIPVILERYKEKQLVPLDKTKFLVPHVM 109	AC Q9PC74;	PRELIMINARY;	PRT;	121 AA.	
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Db	61 SELVKIRRQLQNLNTQAFLLVNVQHSMWSVSTPIADIYEQEKGFLYMWVQSETRG 120	DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)				
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Db	61 SELVKIRRQLQNLNTQAFLLVNVQHSMWSVSTPIADIYEQEKGFLYMWVQSETRG 120	GN 101000H21R1K.				
OS	Mus musculus (Mouse);					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OX	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
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Db	1 MPSDRPKQRRSFADRCKEVQIQRDQHPSKIPVILERYKEKQLVPLDKTKFLVPHVM 60	RC STRAIN=C57BL/6J; TISSUE=Heart;				
QY	1 MPSDRPKQRRSFADRCKEVQIQRDQHPSKIPVILERYKEKQLVPLDKTKFLVPHVM 60	RX MEDLINE=21085650; PubMed=11217851;				
Db	1 MPSDRPKQRRSFADRCKEVQIQRDQHPSKIPVILERYKEKQLVPLDKTKFLVPHVM 60	RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,				
QY	61 SELVKIRRQLQNLNTQAFLLVNVQHSMWSVSTPIADIYEQEKGFLYMWVQSETRG 120	RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,				
Db	61 SELVKIRRQLQNLNTQAFLLVNVQHSMWSVSTPIADIYEQEKGFLYMWVQSETRG 120	RA Iizawa K., Iizawa M., Nishii K., Kiyosawa H., Kondo S., Yamamoto I.,				
QY	61 SELVKIRRQLQNLNTQAFLLVNVQHSMWSVSTPIADIYEQEKGFLYMWVQSETRG 120	RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,				
Db	61 SELVKIRRQLQNLNTQAFLLVNVQHSMWSVSTPIADIYEQEKGFLYMWVQSETRG 120	RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Cassavant T.,				
QY	61 SELVKIRRQLQNLNTQAFLLVNVQHSMWSVSTPIADIYEQEKGFLYMWVQSETRG 120	RA Fleischmann M.J., Gaasterland T., Gissi C., King B., Kochiwa H.,				
Db	61 SELVKIRRQLQNLNTQAFLLVNVQHSMWSVSTPIADIYEQEKGFLYMWVQSETRG 120	RA Kuehl P., Lewis S., Matsu Y., Nikaido I., Pesole G., Quackenbush J.,				
QY	61 SELVKIRRQLQNLNTQAFLLVNVQHSMWSVSTPIADIYEQEKGFLYMWVQSETRG 120	RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,				
Db	61 SELVKIRRQLQNLNTQAFLLVNVQHSMWSVSTPIADIYEQEKGFLYMWVQSETRG 120	RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,				
QY	121 F 121	RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,				
Db	121 F 121	RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,				
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DT 01-MAR-2001 (TREMBlrel. 16, Created)						
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)						
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)						
DE BA34RK17.1.2 (Novel protein similar to MAP1AC3 (Microtubule-associated protein 1A/1B light chain 3) from Rat, isoform 2) (Fragment).						
DE Proteins 1A/1B light chain 3 from Rat, isoform 2) (Fragment).						
GN BA34RK17.1.2						
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OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC europsids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Bahl J.,  
 RA Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,  
 RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,  
 RA Kawai J., Lam B., Lee J.M., Lin J.J., Liu S.X., Miranda M., Narusaka M.,  
 RA Nguyen M., Onodera C.S., Palm J.J., Pham P.K., Quach H.L., Sakurai T.,  
 RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,  
 RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,  
 RA Ecker J.R.;  
 RT "Arabidopsis cDNA clones";  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Yamada K., Bahl J., Chan M.M., Chang C.H., Chang E., Dale J.M.,  
 RA Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,  
 RA Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,  
 RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,  
 RA Kamiya A., Karlin-Neumann G., Kawai J., Lin J.,  
 RA Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,  
 RA Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K.,  
 RA Davis R.W., Ecker J.R., Theologis A.;  
 RT "Full length cDNA of gene At2g45170 (GI:15225418)";  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AF412106; AAL06559.1;  
 DR InterPro; IPR00241; MAPI\_LC3.  
 DR Pfam; PF02951; MAPI\_LC3.  
 DR SEQUENCE 122 AA; 13947 MW; AA504855340CE173 CRC64;  
 SQ

Query Match 36.3%; Score 227; DB 10; Length 122;  
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 Indels 2; Gaps 2;

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 DB 6 FKKSNPLEARMSSESSRRIKEYKDFKIPVVERAKGSDVPEIDKKVLYPAULVGLFVYV 64  
 DR 67 IRRPLQINPTOAFPLVNHMSMWSVSPVIAPIYEQEKEDEGFLYVVAQEFV; 120  
 DR 65 VRKRKLGAEKAIFVFW KNILPTAI MSA1YEHDKDGFGLYMMVSYENFG 117

RP RESULT 13  
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 AC Q8S928; DT 01-JUN-2002 (TREMBL; 21, last sequence update)  
 DT 01-MAR-2003 (TREMBL; 23, last annotation update)  
 DE Autophagy 8a (Autophagy AP-8) (Symbiosis-related like protein).  
 GN ATAF8A OR ATAF8A OR ATAF8B  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Spermatophyta; Magnoliophyta; eudicots; Rosidae;  
 OC europsids II; Brassicales; Brassicaceae; Arabidopsis.  
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 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hanacka H., Noda T., Shitani Y., Sato S., Kato T., Hayashi H.,  
 RA Shibata D., Tabara S., Ohsumi Y.;  
 RT "Disruption or ATAF89 indicates autophagy is involved in leaf  
 senescence and starvation tolerance in higher plant";  
 RT Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RT PubMed=12070171;  
 RA Doelling J.H., Walker J.M., Friedman E.M., Thompson A.R.,  
 RA Vierstra R.D.;  
 RT "The Atg8/12-activating Enzyme AtP7 is Required for Proper Nutrient  
 Recycling and Senescence in Arabidopsis thaliana";  
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 DR InterPro; IPR00241; MAPI\_LC3.  
 DR Pfam; PF02951; MAPI\_LC3; 1  
 DR SEQUENCE 122 AA; 13695 MW; 9F0445B55349B CRC64;  
 SQ

Query Match 36.3%; Score 226; DB 10; Length 122;  
 Best Local Similarity 37.7%; pred. No. 1, 4e-15;  
 Matches 43; Conservative 31; Mismatches 38; Indels 2; Gaps 2;

QY 7 FKKRSFADRCKEVQIQRDQHPSKIPVILEYKCEKJLPVLDKTKFVPHVNMSERVKI 64  
 DB 6 FKSINPLEARMSSESSRRIKEYKDFKIPVVERAKGSDVPEIDKKVLYPAULVGLFVYV 64  
 DR 67 IRRPLQINPTOAFPLVNHMSMWSVSPVIAPIYEQEKEDEGFLYVVAQEFV; 120

